

MEDLINE=93132798; PubMed=8421313;  
Hung C.-H., Lee M.-C., Lee T.C., Lin J.-Y.;  
RT "Primary structure of three distinct isoforms determined by cDNA  
RA sequencing. Conservation and significance.";  
J. Mol. Biol. 229:263-267(1993).  
[2]  
RN SEQUENCE OF 260-527.  
RP  
RC TISSUE=Seed;  
MEDLINE=93169023; PubMed=7763422;  
Kimura M., Sumizawa T., Funatsu G.;  
RA "The complete amino acid sequences of the B-chains of abrin-a and  
RT abrin-b, toxic proteins from the seeds of Abrus precatorius.";  
RL Biosci. Biotechnol. Biochem. 57:166-169(1993).  
CC -!- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN  
SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL  
SUBUNIT BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA.  
CC ABRIN-A IS MORE TOXIC THAN RICIN.  
CC -!- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT  
FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT  
PRECEDES ENDOCYTOSIS.  
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
specific adenosine on the 28S rRNA.  
CC -!- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.  
CC -!- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN  
CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).  
CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-  
INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.  
CC -!- SIMILARITY: Contains 2 ricin B-type lectin domains.  
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EMBL; M98345; AAA32625.1; -.  
DR PIR; S32430; S32430.  
DR HSSP; P11140; 1ABR.  
DR InterPro; IPR000772; Ricin\_B\_lectin.  
DR InterPro; IPR001574; RIP.  
DR Pfam; PF00652; Ricin\_B\_lectin; 6.  
DR Pfam; PF00161; RIP; 1.  
DR PRINTS; PR00396; SHIGARICIN.  
DR SMART; SM00458; RICIN; 2.  
DR PROSITE; PS50231; RICIN\_B\_LECTIN; 2.  
DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
KM Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;  
KW Glycoprotein; Lectin; Pyrrolidone carboxylic acid.  
FT CHAIN 1 250  
FT FT PEPTIDE 251 260 LINKER PEPTIDE.  
FT CHAIN 261 527 ABRIN-B A CHAIN.  
FT FT DOMAIN 272 399 ABRIN-B B CHAIN.  
FT FT DOMAIN 402 526 RICIN B-TYPE LECTIN 1.  
FT FT REPEAT 282 324 RICIN B-TYPE LECTIN 2.  
FT FT REPEAT 325 365 1-ALPHA.  
FT FT REPEAT 368 400 1-BETA.  
FT FT REPEAT 413 448 1-GAMMA.  
FT FT REPEAT 452 491 2-BETA.  
FT FT REPEAT 494 527 2-GAMMA.  
FT FT ACT\_SITE 163 163 BY SIMILARITY.  
FT FT DISULFID 246 268 INTERCHAIN (BY SIMILARITY).  
FT FT DISULFID 285 304 BY SIMILARITY.  
FT FT DISULFID 328 345 BY SIMILARITY.  
FT FT DISULFID 416 429 BY SIMILARITY.  
FT FT DISULFID 455 472 BY SIMILARITY.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID (BY  
SIMILARITY).  
FT FT CARBOHYD 110 110 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT FT CARBOHYD 360 360 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT FT CONFLICT 400 400 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT FT CONFLICT 282 282 N -> D (IN REF. 2).

FT CONFLICT 291 291 D -> N (IN REF. 2).  
 FT CONFLICT 350 351 AE -> PQ (IN REF. 2).  
 FT CONFLICT 378 378 S -> N (IN REF. 2).  
 FT CONFLICT 426 426 L -> M (IN REF. 2).  
 FT CONFLICT 428 428 Y -> D (IN REF. 2).  
 FT CONFLICT 431 431 N -> S (IN REF. 2).  
 FT CONFLICT 434 434 R -> K (IN REF. 2).  
 FT CONFLICT 484 484 N -> S (IN REF. 2).  
 FT CONFLICT 491 491 H -> Y (IN REF. 2).  
 FT CONFLICT 493 493 R -> Q (IN REF. 2).  
 FT CONFLICT 502 502 E -> Q (IN REF. 2).  
 FT CONFLICT 509 509 H -> W (IN REF. 2).  
 FT CONFLICT 513 513 H -> T (IN REF. 2).  
 FT CONFLICT 516 516 H -> T (IN REF. 2).  
 SQ SEQUENCE 527 AA; 59111 MW; 3253AE490C99494A CRC64;  
 Query Match 33.5%; Score 323; DB 1; Length 527;  
 Best Local Similarity 43.9%; Pred. No. 2.1e-22;  
 Matches 83; Conservative 21; Mismatches 59; Indels 16; Gaps 4;  
 QY 5 QYPIINFTAGATVQSYTNFIRAVRGRLT-----VLNRYGLPQINQFIVLSNHA 56  
 Db 1 QDQVIRFTTGGATGSSQYKTEALRQLTGLIHGIPVLPDPTTLOQRNRYISVELSNSD 60  
 QY 57 ELSVTLALDVTNAYVGYRAGNSAYFPHDPNQDAEAIHTLFTDVQNRVYFAFGNYDRL 116  
 Db 61 TESIEAGIDVSNAYVAVRAGNSYFL---RDAPTSASRYLFTGTQ-QYSLRNGSYIDL 116  
 QY 117 EOLAGNLRENIELNGPGLAEISALYYSTGGTQPLTARSFICIMISEAARFOYIEG 176  
 Db 117 ERLARQTRQIPLGLQALRAISFL-----QSGTDDQBIARTLIVIQMASEAARYFISY 172  
 QY 177 EMTRTRYN 185  
 Db 173 RVGVSRITN 181

# RESULT 7 RIP2\_BRYDI

ID RIP2\_BRYDI STANDARD; PRT; 282 AA.  
 AC P98184; Q9S8J0;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Ribosome-inactivating protein bryodin II precursor (rRNA N-Glycosidase) (EC 3.2.2.22) (SD2).  
 OS Bryonia dioica (Red bryonia).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Cucurbitales; Cucurbitaceae; Bryonia.  
 OX NCBI\_TaxID=3652;  
 RN SEQUENCE FROM N.A.  
 RP "Bryodin 2 a ribosome-inactivating protein isolated from the plant Bryonia dioica."  
 RL Patent number US5597569, 28-JAN-1997.  
 RN [2]  
 RP SEQUENCE OF 22-42.  
 RC TISSUE=Root;  
 RX MEDLINE=95151812; PubMed=7849072;  
 RA Siegall C.B., Gawlak S.L., Chace D., Wolff E.A., Mixan B., Marquardt H.;  
 RT "Characterization of ribosome-inactivating proteins isolated from Bryonia dioica and their utility as carcinoma-reactive immunoconjugates."  
 RL Bioconj. Chem. 5:423-429 (1994).  
 CC -!- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS PROTEIN SYNTHESIS IN ANIMAL CELLS (BY SIMILARITY).  
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.  
 CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 1 RIP SUBFAMILY.

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 CC ----- NOT ANNOTATED\_CDS. -----  
 CC EMBL; 134238; -; NOT ANNOTATED\_CDS.  
 DR HSSP; P09989; 1MRJ.  
 DR InterPro; IPR001574; RIP.  
 DR Pfam; PF00161; RIP.1.  
 DR PRINTS; PRO0396; SHIGARICIN.  
 DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
 KW Plant defense; protein synthesis inhibitor; Hydrolase; Toxin;  
 KM Multigene family; Glycoprotein; Signal.  
 FT SIGNAL 1 21 RIBOSOME-INACTIVATING PROTEIN BRYODIN II.  
 FT CHAIN 22 282 BY SIMILARITY.  
 FT ACT\_SITE 183 183 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 25 25  
 SQ SEQUENCE 282 AA; 30754 MW; C52BE2F6A873769C CRC64;  
 Query Match 33.2%; Score 320.5; DB 1; Length 282;  
 Best Local Similarity 46.0%; Pred. No. 1.7e-22;  
 Matches 81; Conservative 24; Mismatches 54; Indels 17; Gaps 7;  
 QY 9 INFTTAGATVQSYTNFIRAVRGRLTV-LPNRYGLPQ-----RFLIVLSNHAELSV 60  
 Db 24 INFLSGLGATGATYKTEIRNLTKLTGTPRVYDIPVLRNAAAGLARFQLVLTNYGESV 83  
 QY 61 TLALDVTNAYVGYRAGNSAYFPHDPNQDAEAIHTLFTDVQNRVYFAFGNYDRLQLA 120  
 Db 84 TVALDVTNAYVGYRAGNSAYFPHDPNQDAEAIHTLFTDVQNRVYFAFGNYDRLQLA 139  
 QY 121 GNL-RENIELNGPGLAEISALYYSTGGTQPLTARSFICIMISEAARFOYIE 175  
 Db 140 GRISRENIELGFSEISSAIGNMFRNP-GTSVP--RAFIVLIQTVSEARFKYIE 191

## RESULT 8

ID NIGB\_SAMNI STANDARD; PRT; 563 AA.  
 AC P33183; P33184; P93542;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Nigrin b precursor (Agglutinin V) (SNAV) [Contains: Nigrin b A chain (rRNA N-glycosidase) (EC 3.2.2.22); Nigrin b chain].  
 OS Sambucus nigra (European elder).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; Campanulids; Dipsacales; Adoxaceae; Sambucus.  
 OX NCBI\_TaxID=4202;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Bark;  
 RX MEDLINE=96215449; PubMed=8647092;  
 RA Van Damme E.J., Barre A., Rouge P., Van Leuven F., Peumans W.J.;  
 RT "Characterization and molecular cloning of Sambucus nigra agglutinin V (nigrin b), a GalNAc-specific type-2 ribosome-inactivating protein from the bark of elderberry (Sambucus nigra).";  
 RL Eur. J. Biochem. 237:505-513 (1996).  
 RN [2]  
 RP SEQUENCE OF 26-49 AND 298-321.  
 RC TISSUE=Bark;  
 RX MEDLINE=94003077; PubMed=8400135;  
 RA Girbes T., Citores L., Ferreras J.M., Rojo M.A., Iglesias R., Munoz R., Arias F.J., Calonge M., Garcia J.R., Mendez E.;  
 RT "Isolation and partial characterization of nigrin b, a non-toxic novel type 2 ribosome-inactivating protein from the bark of Sambucus nigra L.";  
 RL Plant Mol. Biol. 22:1181-1186 (1993).  
 CC -!- FUNCTION: NON-TOXIC TYPE 2 RIP WHICH STRONGLY INHIBITS MAMMALIAN



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CC or send an email to license@sib.ch).
CC -----
DR EMBL; I24020; -; NOT_ANNOTATED_CDS.
DR PIR; S16491.
DR PDB; 1BRY; 04-MAR-98.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA RICIN; 1.
KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin;
KW 3D-structure; Multigene family; Glycoprotein; Signal.
FT SIGNAL 1 23
FT CHAIN 24 270 RIBOSOME-INACTIVATING PROTEIN BRYODIN I.
FT PROPEP 271 290 MISSING IN MATURE PROTEIN.
FT ACT_SITE 183 183 BY SIMILARITY.
FT ACT_SITE 212 212
FT CARBOHYD 214 214 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 250 250 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MUTAGEN 212 212 E->K; REDUCES ACTIVITY 10-FOLD.
FT CONFLICT 61 65 RSSIS -> LRHXI (IN REF. 3).
FT STRAND 25 28
FT TURN 30 31
FT HELIX 34 46
FT TURN 47 47
FT STRAND 50 54
FT TURN 55 56
FT STRAND 57 60
FT HELIX 66 69
FT STRAND 70 76
FT TURN 78 79
FT STRAND 82 88
FT TURN 89 92
FT STRAND 93 99
FT TURN 100 101
FT STRAND 102 105
FT HELIX 109 114
FT TURN 115 117
FT TURN 120 121
FT STRAND 124 127
FT HELIX 134 141
FT TURN 142 142
FT HELIX 145 147
FT STRAND 150 150
FT HELIX 152 163
FT TURN 164 165
FT HELIX 167 186
FT STRAND 187 187
FT HELIX 188 196
FT STRAND 202 202
FT HELIX 206 213
FT TURN 214 214
FT HELIX 215 225
FT TURN 226 230
FT STRAND 231 239
FT TURN 241 242
FT STRAND 245 250
FT TURN 251 252
FT HELIX 254 257
FT TURN 258 259
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FT STRAND 263 263
FT HELIX 266 268
SQ SEQUENCE 290 AA; 31788 MW; E966CD9C031A42DB CRC64;

Query Match 31.6%; Score 305; DB 1; Length 290;
Best Local Similarity 35.7%; Pred. No. 4.8e-21;
Matches 65; Conservative 45; Mismatches 56; Indels 16; Gaps 4;

OY 9 INFTTAGVQSYTFIRAVRGLTVLPNRVCLPI-----NQRFILVELSNHAEISVT 61
DB 25 VSRFLSGATTTSYGVFIKNLRALPYRKYVNIPLRRSSISGSGRYTLHLTNVADETIS 84
OY 62 LALDVTNAYVVGYNAGSAYFFHPDNPQEDA-EAITHLFTDVQNRVTFAPGNGYDRLEQLA 120

Db 85 VADVTVNYIMGLAGVSYFF--NEASATEAKVFKDAKKKVTLPYSNVERLQTAA 141
OY 121 GNLENIELGNGLPELEAISALYYSTGTGTLPTLARSFIICQMISEARFOVIEGEMRT 180
Db 142 GKIRENIPGLPALDGAITLYYVTAS-----SAASALLVLIQSTABSARYKFTIEQIGK 196
OY 181 RI 182
Db 197 RV 198

RESULT 10
ABRA ABRPR STANDARD; PRT; 528 AA.
AC P11140; P28589;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Abrin-a precursor [Contains: Abrin-a A chain (rRNA N-glycosidase)
DE (EC 3.2.2.22); Abrin-a B chain].
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
OX NCBI_TaxID=3916;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93132798; PubMed=8421313;
RA Hung C.-H., Lee M.-C., Lee T.-C., Lin J.-Y.;
RT "Primary structure of three distinct isoabrin determined by cDNA
RL J. Mol. Biol. 229:263-267 (1993).
RN [2]
RP SEQUENCE OF 1-251.
RC TISSUE=Seed;
RA Funatsu G., Taguchi Y., Kamenosono M., Yanaka M.;
RT "The complete amino acid sequence of the A-chain of abrin-a, a toxic
RL Agric. Biol. Chem. 52:1095-1097 (1988).
RN [3]
RP SEQUENCE OF 1-251 FROM N.A.
RC TISSUE=Leaf;
RX MEDLINE=91201329; PubMed=2016300;
RA Evensen G., Mathiesen A., Sundan A.;
RT "Direct molecular cloning and expression of two distinct abrin
RL A-chains."
RN [4]
RP J. Biol. Chem. 266:6848-6852 (1991).
RP SEQUENCE OF 262-528.
RX MEDLINE=92371656; PubMed=1505674;
RA Chen Y.-L., Chow L.-P., Tsugita A., Lin J.-Y.;
RT "The complete primary structure of abrin-a B chain."
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.14 ANGSTROMS).
RX MEDLINE=95333188; PubMed=7608980;
RA Tahirov T.H., Lu T.-H., Liaw Y.-C., Chen Y.-L., Lin J.-Y.;
RT "Crystal structure of abrin-a at 2.14 A."
RL J. Mol. Biol. 250:354-367 (1995).
CC -!- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN
CC SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
CC SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA.
CC ABRIN-A IS MORE TOXIC THAN RICIN.
CC -!- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT
CC FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT
CC PRECEDES ENDOCYTOSIS.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -!- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
CC -!- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN
CC CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-
```

CC INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.  
 CC -!- SIMILARITY: Contains 2 ricin B-type lectin domains.  
 CC  
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 CC -----  
 CC EMBL; M98344; AAA32624.1; ALT INIT.  
 CC EMBL; X54872; -; NOT ANNOTATED\_CDS.  
 CC PIR; S32429; TZLSA.  
 CC PDB; 1ABR; 07-FEB-95.  
 CC InterPro; IPR000772; Ricin\_B\_lectin.  
 CC InterPro; IPR001574; RIP.  
 CC Pfam; PF00652; Ricin\_B\_lectin; 6.  
 CC Pfam; PF00161; RIP; 1.  
 CC PRINTS; PR00396; SHIGARICIN.  
 CC SMART; SM00458; RICIN; 2.  
 CC PROSITE; PS00231; RICIN B LECTIN; 2.  
 CC PROSITE; PS00275; SHIGA\_RICIN; 1.  
 CC Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;  
 CC Glycoprotein; Lectin; 3D-structure; Pyrrolidone carboxylic acid.  
 CC CHAIN 1 251  
 CC PEPTIDE 252 261  
 CC CHAIN 262 528  
 CC DOMAIN 273 400  
 CC MAIN 403 527  
 CC REPEAT 283 325  
 CC REPEAT 326 366  
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 CC ACT SITE 164 164  
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 CC DISULFID 286 305  
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 FT STRAND 501

Query Match 31.5%; Score 303.5; DB 1; Length 528;  
 Best Local Similarity 41.1%; Pred. No. 1.4e-20;  
 Matches 76; Conservative 26; Mismatches 64; Indels 19; Gaps 5;

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QY 9 INFETAGATVQSYNTNFIKAVRGRL-----TVLPNRVGLPINQRFILVLSNHAELSV 60
Db 5 IKFSTEGATQSYKQFIALRERURGGIHLDPVLPDPTTLQERNKRYITVLSNSTDTSI 64
QY 61 TLALDVTNAYVVGVRAGNSAYFFH--PDNQDAEAIHTLFTDVQNRVYTFAGGNYDRLEQ 118
Db 65 EVGIDVTNAYVVGVRAGTQSYFLRDAPSSASD-----YLFCT--DQHSLPFGVTGDLER 118
QY 119 LAGNRENIELNGPLLEBAISALYYSTGGTQLPPLARSFFIICIMISEAARFQVIEGEM 178
Db 119 WAHOSRQOIPGLQALTHGIS----PFRSGGNDNEEKARTLIIQWVAEAAARFRYISNRV 175
QY 179 RTRIR 183
Db 176 RVSIQ 180

RESULT 11
ID RIPB_LUCFY STANDARD; PRT; 250 AA.
AC P22851;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribosome-inactivating protein luffin-B (rRNA N-glycosidase)
DE (EC 3.2.2.22).
OS Luffa cylindrica (Smooth loofah) (Sponge gourd).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Luffa.
OX NCBI_TaxID=3670;
RN [1]
RP SEQUENCE
RC TISSUE=Seed;
RX MEDLINE=91248488; PubMed=1368666;
RA Islam M.R., Hirayama H., Funatsu G.;
RT "Complete amino acid sequence of luffin-b, a ribosome-inactivating
RL protein from sponge gourd (Luffa cylindrica) seeds.";
RL Agric. Biol. Chem. 55:229-238(1991).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
DR PIR; JN0108; JN0108.
DR HSSP; P16094; 1AHC.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
KW Toxin.
FT ACT SITE 160 160 BY SIMILARITY.
FT SEQUENCE 250 AA; 27293 MW; F01A8DC8A107800 CRC64;
Query Match 30.4%; Score 293.5; DB 1; Length 250;
Best Local Similarity 33.7%; Pred. No. 4.7e-20;
Matches 63; Conservative 46; Mismatches 57; Indels 21; Gaps 4;

QY 9 INFETAGATVQSYNTNFIKAVRGRL-----TVLPNRVGLPINQRFILVLSNHAEL 58
Db 3 VSFSLSGADSKSYKFTALRKALPKSKVSNIPLLPSASGA---SRVILMQLSNYDAK 59
QY 59 SVTLALDVTNAYVVGVRAGNSAYFFH--PDNQDAEAIHTLFTDVQNRVYTFAGGNYDRLEQ 118
Db 60 ALTMADVTNVMYGLVNSTSYF---ANESDAKLASQYVFKGSTLVLTIPYSGNVERLQN 116
QY 119 LAGNRENIELNGPLLEBAISALYYSTGGTQLPPLARSFFIICIMISEAARFQVIEGEM 178
Db 117 AAGKIREKIPGLGRALDSALTSIFHYDS-----TAAAAAFVLVLTQTAASGRFKIEGQI 171
QY 179 RTRIR 185
Db 172 IERIPKN 178

```

## RESULT 12

```

ID RIP1_CUCFI STANDARD; PRT; 286 AA.
AC Q9PFX4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative ribosome-inactivating protein precursor (rRNA N-glycosidase)
DE (EC 3.2.2.22).
OS Cucumis figareii.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
OX NCBI_TaxID=131071;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada T., Ohki S.T., Osaki T.;
RT "Cloning and analysis of a cDNA coding a putative ribosome-
RT inactivating protein from Cucumis figareii.";
RL Plant Biotechnol. 17:337-340(2000).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB045560; BAB19677.1; -.
CC HSSP; P16094; 1AHC.
CC InterPro; IPR001574; RIP.
CC Pfam; PF00161; RIP; 1.
CC PRINTS; PR00396; SHIGARICIN.
CC PROSITE; PS00275; SHIGA_RICIN; 1.
KW Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
KW Toxin; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 286 PUTATIVE RIBOSOME-INACTIVATING PROTEIN.
FT ACT SITE 185 185 BY SIMILARITY.
FT CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 286 AA; 31771 MW; 4BFD4966E604DA41 CRC64;
Query Match 29.2%; Score 281.5; DB 1; Length 286;
Best Local Similarity 32.4%; Pred. No. 7.1e-19;
Matches 60; Conservative 46; Mismatches 64; Indels 15; Gaps 3;

QY 9 INFETAGATVQSYNTNFIKAVRGRLTVLPNRVGLPI-----NORFILVLSNHAELSVT 61
Db 28 VKFSLSGNHSKYSKFTSMRNALPNAGDYNIPLLVPISGSRRYILMQLSNYEGNTIT 87
QY 62 LALDVTNAYVVGVRAGNSAYFFH--PDNQDAEAIHTLFTDVQNRVYTFAGGNYDRLEQ 121
Db 88 MANDVTNVMYGLVNSTSYFF---NETDAQASKFVFOGTSKITLPSGNYKQLQSVAR 144
QY 122 NLRENIELNGPLLEBAISALYYSTGGTQLPPLARSFFIICIMISEAARFQVIEGEMRTR 181
Db 145 KERDSIPGLGRALDSALTSIYYVDSRSGAPI-----AFVLVIQTAAEAARYKIEQI 199
QY 182 IRYNR 186
Db 200 ISVSK 204

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## RESULT 13

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RIPA_LUFYCY
ID RIPA_LUFYCY STANDARD; PRT; 277 AA.
AC Q00465;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ribosome-inactivating protein luffin-alpha precursor (rRNA
N-glycosidase) (EC 3.2.2.22).
OS Momordica balsamina (Bitter melon) (Sponge gourd).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotsids I; Cucurbitales; Cucurbitaceae; Luffa.
OX NCBI_TaxID=3670;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Seed;
RX MEDLINE=92288316; PubMed=1600156;
RA Kataoka J., Habuka N., Miyano M., Masuta C., Koiwai A.;
RT "Nucleotide sequence of cDNA encoding alpha-luffin, a ribosome-
inactivating protein from Luffa cylindrica."
RL Plant Mol. Biol. 18:1199-1202(1992).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; X62371; CAA44229.1; -
CC PIR; S22494; S22494.
CC HSP; P16094; 1AHC.
CC InterPro; IPR001574; RIP.
CC PRINTS; PR00396; SHIGARICIN.
CC PROSITE; PS00275; SHIGA_RICIN; 1.
CC Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
CC Toxin; Signal.
CC SIGNAL 1 19 RIBOSOME-INACTIVATING PROTEIN LUFFIN-
CC CHAIN 20 277 ALPHA.
CC ACT_SITE 179 179 BY SIMILARITY.
CC SEQUENCE 277 AA; 30212 MW; EAL7FC27998C25AC CRC64;
Query Match 28.4%; Score 274.5; DB 1; Length 277;
Best Local Similarity 33.3%; Pred. No. 3e-18;
Matches 63; Conservative 42; Mismatches 61; Indels 23; Gaps 5;
QY 9 INFTAGATVQSYTNFIRAVRGRLTVLPNRVGLPIN-----QRFILVELSNHAE 57
Db 22 VRESLSSGSSSTYSKFIGDLR---KALPSN-GTVYNTLLSSAGSRVLTMTLSNYDG 77
QY 58 LSVTLALDVTNAVVGVRAGNSAYFFHPDNOEAEATHLFTDVQNRYPFAFGNVDRL 117
Db 78 KAITVAADVTVNVIMGLVNSTGYFF---NESDAKLASQVVRKSTIVTLPYSGNVEK 134
QY 118 QLAGNRLNLELNGPLGLEEALSALYYSTGGTQLPTLARSFFIICIMISEAARFQIE 177
Db 135 TAAGKIREKIPGLGPPALDSAITLFLHYDS-----TAAAAAFLVIIQTAAEAPK 189
QY 178 MRTRIRYN 186
Db 190 IIERISNQ 198
RESULT 14
RIP2_MOMBA STANDARD; PRT; 286 AA.
ID RIP2_MOMBA

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P29339;
AC 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ribosome-inactivating protein momordin II precursor (rRNA
N-glycosidase) (EC 3.2.2.22).
OS Momordica balsamina (Bitter melon) (Sponge gourd).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotsids I; Cucurbitales; Cucurbitaceae; Momordica.
OX NCBI_TaxID=3672;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Seed;
RX MEDLINE=93027170; PubMed=1408771;
RA Ortigao M., Better M.;
RT "Momordin II, a ribosome inactivating protein from Momordica
balsamina, is homologous to other plant proteins."
RL Nucleic Acids Res. 20:4662-4662(1992).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
CC
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CC
CC EMBL; Z12175; CAA78166.1; -
CC PIR; S25560; S25560.
CC PDB; 1CF5; 07-JUN-99.
CC InterPro; IPR001574; RIP.
CC Pfam; PF00161; RIP; 1.
CC PRINTS; PR00396; SHIGARICIN.
CC PROSITE; PS00275; SHIGA_RICIN; 1.
CC Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin; Signal;
CC 3D-structure.
CC SIGNAL 1 23 RIBOSOME-INACTIVATING PROTEIN MOMORDIN
CC CHAIN 24 286 II.
CC ACT_SITE 181 181 BY SIMILARITY.
CC SEQUENCE 286 AA; 32031 MW; 3B89FFIAEGB25986 CRC64;
Query Match 28.4%; Score 274; DB 1; Length 286;
Best Local Similarity 34.0%; Pred. No. 3.5e-18;
Matches 65; Conservative 39; Mismatches 71; Indels 16; Gaps 4;
QY 2 VPKQPIINFTAGATVQSYTNFIRAVRGRLTVLPNRVGLPI-----NQRFILVELSN 54
Db 18 VPTAKGVNFDLSTAKTYTKFIEDFRATLPFSHKVVDIPLLYSTISDRRFLDLTS 77
QY 55 HAEISVTLALDVTNAVVGVRAGNSAYFFHPDNOEAEATHLFTDVQNRYPFAFGNVD 114
Db 78 YAYETISVAIDVTNVVAVRTDVSYPF---KESPPRAYNTLFXGTR-KITLPYTGNYE 133
QY 115 RLEQLAGNRLNLELNGPLGLEEALSALYYSTGGTQLPTLARSFFIICIMISEAARFQ 174
Db 134 NLQTAHAKIRENIDLGLPALSSAITLFLFYNA-----QSAPSAALLVLIQTAAEAPK 188
QY 175 EGMETRIYRN 185
Db 189 ERHVAKYVATN 199
RESULT 15
RIP1_MOMCH STANDARD; PRT; 286 AA.
ID RIP1_MOMCH
AC P16094; P24697;
DT 01-APR-1990 (Rel. 14, Created)

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PDB; LAHC; 22-JUN-94.
PDB; IMOM; 31-MAY-94.
PDB; IMRG; 07-FEB-95.
PDB; IMRH; 07-FEB-95.
PDB; IMRI; 07-FEB-95.
PDB; IP8Q; 21-NOV-01.
GlycoSuiteDB; P16094; --
InterPro; IPR001574; RIP.
Fram; PR00161; RIF; 1.
PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA RICIN; 1.
KW plant defense; protein synthesis inhibitor; Hydrolase; Toxin; Signal;
XW Glycoprotein; 3D-structure.
SIGNAL 1 23
FT CHAIN 24 269
FT PROPEP 270 286
FT ACT SITE 183 183
FT CARBOHYD 250 250
FT STRAND 25 28
FT HELIX 34 47
FT STRAND 50 54
FT TURN 55 56
FT STRAND 57 60
FT HELIX 66 69
FT STRAND 70 76
FT TURN 78 79
FT STRAND 82 88
FT TURN 89 92
FT STRAND 93 99
FT TURN 100 101
FT STRAND 102 105
FT HELIX 109 114
FT TURN 115 117
FT TURN 120 121
FT STRAND 124 127
FT HELIX 134 141
FT HELIX 145 147
FT STRAND 150 150
FT HELIX 152 162
FT TURN 163 163
FT HELIX 167 186
FT STRAND 187 187
FT HELIX 188 195
FT TURN 196 197
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FT HELIX 206 225
FT TURN 226 230
FT STRAND 231 238
FT TURN 240 241
FT STRAND 246 250
FT TURN 251 252
FT HELIX 254 258
FT TURN 259 259
FT STRAND 260 260
FT STRAND 263 263
FT HELIX 266 268
SQ SEQUENCE 286 AA; E1B013ABEBC216CF CRC64;
Query Match 28.3%; Score 273; DB 1; Length 286;
Best Local Similarity 34.8%; Pred No. 4.3e-18;
Matches 63; Conservative 40; Mismatches 62; Indels 16; Gaps 4
QY 9 INFETAGATGVSYNFIRAVRGRITVLPNRVGLPI-----NORFILVELSNHAEISVT 61
DB 25 VSRFLSGADPSYGMFIKDLNALPFREKVNIPLLPSSVGAGRYLLMHLFNVDKTIIT 84
QY 62 LALDVNTAYVGVYRAGNSAYFFHPDNQEDAE-AITHLFTDVQNRYTFAPGGNYDRLEQLA 120
DB 85 VAVDTNVTVINGYLADTTTSYFF--NEPAAEIASQYVFRDARKKITLPYSGNRYERLQIAA 141
QY 121 GNLRNIELGNGLPEEAISALYYSTGTQTPLTARSFLIICIOMISEARFYIEGEMET 180



Db 142 GKPREKIPIGLPALDSAISTLLHYDS-----TAAGALLVLIQTAAARFKYIEQQIOE 196

QY 181 R 181

Db 197 R 197

Search completed: February 10, 2004, 16:23:25  
Job time : 7.27131 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:17:00 ; Search time 25.0852 Seconds  
(without alignments)  
1933.961 Million cell updates/sec

Title: US-10-083-336A-8

Perfect score: 965

Sequence: 1 MVPKQYPIINFATTAGATVQS.....ARFQYIEGEMRIIRYNRRS 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_23.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	941	97.5	541	Q41174	ricinus com
2	374.5	38.8	580	Q94BW3	cinnaomom
3	372.5	38.6	580	Q94BW4	cinnaomom
4	370.5	38.4	581	Q94BW5	cinnaomom
5	368.5	38.2	549	Q9FV22	cinnaomom
6	334	34.6	289	Q94KE4	trichosanth
7	332	34.4	289	Q41216	trichosanth
8	329.5	34.1	563	Q04367	sambucus ni
9	326	33.8	247	Q9LRE3	trichosanth
10	323.5	33.5	564	Q9AVR2	sambucus eb
11	318.5	33.0	528	Q06076	abrus preca
12	317	32.8	270	Q8LPV7	trichosanth
13	310.5	32.2	252	Q38760	abrus preca
14	307.5	31.9	563	Q94552	sambucus ni
15	307.5	31.9	563	Q8GT32	sambucus ni
16	305	31.6	270	Q41611	trichosanth

17	303.5	31.5	252	10	Q38761	abrus preca
18	302	31.3	565	10	Q04071	sambucus ni
19	300.5	31.1	278	10	Q00980	luffa cylin
20	298.5	30.9	547	10	Q9M6B9	abrus preca
21	297.5	30.8	251	10	Q96236	abrus preca
22	296.5	30.7	251	10	Q96237	abrus preca
23	293.5	30.4	566	10	Q04072	sambucus ni
24	290.5	30.1	251	10	Q96235	abrus preca
25	273	28.3	264	10	Q9FSH2	momordica c
26	272	28.3	570	10	Q41358	sambucus ni
27	272	28.2	286	10	Q9FUV7	momordica c
28	271	28.1	592	10	Q8W2E7	iris hollan
29	270	28.0	249	10	Q8LKQ5	viscum albu
30	267	27.7	286	10	Q41257	viscum albu
31	267	27.7	570	10	Q22415	sambucus ni
32	266.5	27.6	604	10	Q9M654	polygonatum
33	263	27.3	565	10	Q8W243	viscum albu
34	260	26.9	254	10	Q8LKQ6	viscum albu
35	260	26.9	573	10	Q8W2E8	iris hollan
36	259	26.8	251	10	Q8LKQ4	viscum albu
37	259	26.8	293	10	Q8S452	jatropha cu
38	259	26.8	569	10	P93543	sambucus ni
39	253	26.2	531	10	Q8RXH6	viscum albu
40	251	26.0	249	10	Q8RXH7	viscum albu
41	247	25.6	258	10	Q8S9E4	gelonium mu
42	247	25.6	293	10	Q8VT00	jatropha cu
43	246.5	25.5	203	10	Q8RY69	gynostemma
44	246.5	25.5	275	10	Q8HIY4	gynostemma
45	245.5	25.4	603	10	Q9M653	polygonatum

## ALIGNMENTS

### RESULT 1

Q41174  
ID Q41174 PRELIMINARY; PRT; 541 AA.  
AC Q41174;  
DT 01-NOV-1996 (TRENBLrel. 01, Created)  
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
DE Proridin A chain (EC 3.2.2.22) (rRNA N-glycosidase)  
DE (Fragment).  
OS Ricinus communis (Castor bean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicotyledons;  
OC eucotsids I; Malpighiales; Euphorbiaceae; Ricinus.  
OX NCBI\_TaxID=3988;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92338377; PubMed=1633311;  
RA Roberts L.M., Tregear J.W., Lord J.M.;  
RT "Molecular cloning of ricin";  
RL Targeted Diagn. Ther. 7:81-97(1992).  
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
SPECIFIC ADENOSINE ON THE 28S RRNA.  
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
EMBL; S40366; AB22582.1; -;  
DR HSSP; P02879; 1BR6.  
DR InterPro; IPR000772; Ricin\_B\_lectin.  
DR InterPro; IPR001574; RIP.  
DR InterPro; IPR001400; Somatotropin.  
DR Pfam; PF00652; Ricin\_B\_lectin; 6.  
DR Pfam; PF00161; RIP; 1.  
DR PRINTS; PR00396; SHIGARICIN.  
DR SMART; SM00458; RICIN; 2.  
DR PROSITE; PS02031; RICIN\_B\_LECTIN; 2.  
DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
DR PROSITE; PS00338; SOMATOTROPIN\_2; 1.  
KW Hydrolase; Toxin.  
FT NON TER 1  
SEQUENCE 541 AA; 60281 MW; 2B7B2CDEF1F2E9D9 CRC64;

Query Match 97.5%; Score 941; DB 10; Length 541;  
 Best Local Similarity 94.9%; Pred. No. 2.4e-81;  
 Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINOQRFILVEL 52  
 DB 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINOQRFILVEL 62

QY 53 SNHAELSVTLALDVNTNAYVGYRAGNSAYFFHPDNOQDAEAITHLFTDQVQNYTFAFGGN 112  
 DB 63 SNHAELSVTLALDVNTNAYVGYRAGNSAYFFHPDNOQDAEAITHLFTDQVQNYTFAFGGN 122

QY 113 YDRLEQLAGNLRENIELGNGLPLEAISAALYYSTGGTQLPILARSFFIICQMISEAARFQ 172  
 DB 123 YDRLEQLAGNLRENIELGNGLPLEAISAALYYSTGGTQLPILARSFFIICQMISEAARFQ 182

QY 173 YIEGEMTRIRYNRRS 188  
 DB 183 YIEGEMTRIRYNRRS 198

## RESULT 2

Q94BW3 ID Q94BW3 PRELIMINARY; PRT; 580 AA.  
 AC Q94BW3;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Type 2 ribosome-inactivating protein cinnamomin III precursor  
 DE (EC 3.2.2.22) (rRNA N-glycosidase).  
 OS Cinnamomum camphora (Camphor tree).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.  
 OX NCBI\_TaxID=13429;  
 RN [1]

SEQUENCE FROM N.A.  
 Yang Q., Gong Z.Z., Liu W.Y.;  
 "Molecular cloning of three type 2 RIP (ribosome-inactivating protein)  
 genes encoding cinnamomin proteins and study of their expression  
 patterns";  
 Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 CC SPECIFIC ADENOSINE ON THE 28S RRNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 DR EMBL: AY039803; AAK82460.1;  
 DR InterPro: IPR000772; Ricin\_B\_lectin.  
 DR InterPro: IPR001574; RIP.  
 DR Pfam: PF00652; Ricin\_B\_lectin; 6.  
 DR Pfam: PF00161; RIP; 1.  
 DR PRINTS; PR00396; SHIGARICIN.  
 DR SMART; SM00458; RICIN; 2.  
 DR PROSITE; PS0231; RICIN\_B\_LECTIN; 2.  
 KW Hydrolase; Signal; Toxin.  
 FT SIGNAL 1 32 POTENTIAL.  
 FT CHAIN 33 580 TYPE 2 RIBOSOME-INACTIVATING PROTEIN  
 FT CINNAMOMIN III.  
 SQ SEQUENCE 580 AA; 64421 MW; 940D10F01E7FB558 CRC64;

Query Match 38.8%; Score 374.5; DB 10; Length 580;  
 Best Local Similarity 48.1%; Pred. No. 3.7e-27;  
 Matches 90; Conservative 26; Mismatches 56; Indels 15; Gaps 5;

QY 6 YPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINOQRFILVELSN-H 55  
 DB 33 YQVTFITTKNATKTSYQFIEALRAQLASGEHPHGVMDGSGVTPDSKRFILVELSNWA 92

QY 56 AELSVTLALDVNTNAYVGYRAGNSAYFFHPDNOQDAEAITHLFTDQVQNYTFAFGGN 115  
 DB 93 ADSPTVLADVNTNAYVGYRAGNSAYFFHPDNOQDAEAITHLFTDQVQNYTFAFGGN 149

QY 116 LEQLAGNLRENIELGNGLPLEAISAALYYSTGGTQLPILARSFFIICQMISEAARFQ 175  
 DB 150 LERVAGERREIEILLGMDPLENALSAL--NQORALARSLLIVIQMVAEAVRRFRFIE 207

QY 176 GEMRTIRI 182  
 DB 208 YRVRESI 214

## RESULT 3

Q94BW4 ID Q94BW4 PRELIMINARY; PRT; 580 AA.  
 AC Q94BW4;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Type 2 ribosome-inactivating protein cinnamomin II precursor  
 DE (EC 3.2.2.22) (rRNA N-glycosidase).  
 OS Cinnamomum camphora (Camphor tree).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.  
 OX NCBI\_TaxID=13429;  
 RN [1]

SEQUENCE FROM N.A.  
 Yang Q., Gong Z.Z., Liu W.Y.;  
 "Molecular cloning of three type 2 RIP (ribosome-inactivating protein)  
 genes encoding cinnamomin proteins and study of their expression  
 patterns";  
 Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 CC SPECIFIC ADENOSINE ON THE 28S RRNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 DR EMBL: AY039802; AAK82459.1;  
 DR InterPro: IPR000772; Ricin\_B\_lectin.  
 DR InterPro: IPR001574; RIP.  
 DR Pfam: PF00652; Ricin\_B\_lectin; 6.  
 DR Pfam: PF00161; RIP; 1.  
 DR PRINTS; PR00396; SHIGARICIN.  
 DR SMART; SM00458; RICIN; 2.  
 DR PROSITE; PS0231; RICIN\_B\_LECTIN; 2.  
 KW Hydrolase; Signal; Toxin.  
 FT SIGNAL 1 32 POTENTIAL.  
 FT CHAIN 33 580 TYPE 2 RIBOSOME-INACTIVATING PROTEIN  
 FT CINNAMOMIN II.  
 SQ SEQUENCE 580 AA; 64265 MW; 37E4289ECCE0CBFF CRC64;

Query Match 38.6%; Score 372.5; DB 10; Length 580;  
 Best Local Similarity 47.8%; Pred. No. 5.7e-27;  
 Matches 89; Conservative 27; Mismatches 56; Indels 15; Gaps 5;

QY 6 YPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPI-----NORFILVELSN-H 55  
 DB 33 YQVTFITTKNATKTSYQFIEALRAQLASGEHPHGVMDGSGVTPDSKRFILVELSNWA 92

QY 56 AELSVTLALDVNTNAYVGYRAGNSAYFFHPDNOQDAEAITHLFTDQVQNYTFAFGGN 115  
 DB 93 ADSPTVLADVNTNAYVGYRAGNSAYFFHPDNOQDAEAITHLFTDQVQNYTFAFGGN 149

QY 116 LEQLAGNLRENIELGNGLPLEAISAALYYSTGGTQLPILARSFFIICQMISEAARFQ 175  
 DB 150 LERVAGERREIEILLGMDPLENALSAL--WISNLNQRALARSLLIVIQMVAEAVRRFRFIE 207

## RESULT 4

Q94BW5 ID Q94BW5 PRELIMINARY; PRT; 581 AA.  
 AC Q94BW5;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Type 2 ribosome-inactivating protein cinnamomin I precursor  
 DE (EC 3.2.2.22) (rRNA N-glycosidase).

DR	InterPro; IPR000772; Ricin_B_lectin.	
DR	InterPro; IPR001574; RIP.	
DR	Pfam; PF00652; Ricin_B_lectin; 5.	
DR	Pfam; PF00161; RIP; 1.	
DR	PRINTS; PR00396; SHIGARICIN.	
DR	SMART; SM00458; RICIN; 2.	
DR	PROSITE; PS00231; RICIN_B_LECTIN; 2.	
KW	Hydrolase; Toxin.	
FT	NON_TER	1
SQ	SEQUENCE	549 AA; 60648 MW; 02607FE607CA44B0 CRC64;
	Query Match	38.2%; Score 368.5; DB 10; Length 549;
	Best Local Similarity	48.1%; Pred. No. 1.3e-26;
	Matches	30; Conservative 25; Mismatches 57; Indels 15; Gaps 5
QY	6	YPIINTTAGATVQSYTNFIRAVGRILT-----VLNRRVGLPQNORFILVELSN-H 55
Db	1	YQVTVFTTKATTSYTFQIEALRAQLASGEPHGIPMRERSTVPDSKGFILVELSNWA 60
QY	56	AELSVTALDVTNAYVYGRAGNSAYFFHDPNOEDAEAITHLFTDVQNRVTFARGGNYDR 115
Db	61	ADSPVLADVNTNAYVYVATGSCFQSFRENDPD--PAIENLPDTK-RYTFPPSGSYTD 117
QY	116	LEQAGLNRENIELGNGLPEAFISALYYTGTGQTPLTARSLFTICQMISEAARFOYIE 175
Db	118	LEGVAGERREIILGMDPLENAISALWISNL--NQQRALARSLIVVQVAEVRFRFIE 175
QY	176	GEMRTRI 182
Db	176	YRVGRSI 182
RESULT 6		
Q94KE4		
ID	Q94KE4	PRELIMINARY; PRT; 289 AA.
AC	Q94KE4;	
DT	01-DEC-2001	(TrEMBLrel. 19, Created)
DT	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)
DE	01-MAR-2003	(TrEMBLrel. 23, Last annotation update)
DE	Trichosanthin precursor	(EC 3.2.2.22) (rRNA N-glycosidase).
GN	TCS.	
OS	Trichosanthes kirilowii	(Mongolian snake-gourd).
OC	Rukaryota; Viridiplantae;	Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta;	eudicotyledons; core eudicots; Rosidae;
OC	eurosid I; Cucurbitales;	Cucurbitaceae; Trichosanthes.
OX	NCBI_TaxID=3677;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RL	Yuan H., Wang L., Wang Y., An C., Chen Z.;	
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.	
CC	-1- CATALYTIC ACTIVITY: ENDHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE	
CC	SPECIFIC ADENOSINE ON THE 28S RRNA.	
CC	-1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.	
DR	EMBL; AF367252; AAK52960.1; -.	
DR	InterPro; IPR001574; RIP.	
DR	Pfam; PF00161; RIP; 1.	
DR	PRINTS; PR00396; SHIGARICIN.	
DR	PROSITE; PS00275; SHIGA RICIN; 1.	
DR	KW	Hydrolase; Signal; Toxin.
FT	SIGNAL	1 23
FT	CHAIN	24 270
FT	CHAIN	24 270
SQ	SEQUENCE	289 AA; 31706 MW; A6DS602549CA5657 CRC64;
	Query Match	34.6%; Score 334; DB 10; Length 289;
	Best Local Similarity	38.9%; Pred. No. 1e-23;
	Matches	72; Conservative 42; Mismatches 49; Indels 22; Gaps 5
QY	9	INTTAGATVQSYTNFIRAVGRILTVPN-----RVGLINQRFILVELSNHAEL 58
Db	25	VSFRLSGATSSSYGVFVLSNLR---KAPNRRKGLVDIFLLRSSLPGSQRYALHITNYADE 81
QY	59	SVTIALDVTNAYVYGRAGNSAYFFHDPNOEDA-EAITHLFTDVQNRVTFARGGNYDRLE 117

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Db      82 TTSVAIDVTNVYMGVRAGDTSYFF---NEASATEAAKVFKDSMRKLTLPVSGNYERLQ 138
QY      118 QLAGNLRNIELNGPLEEAISALYYSTGQTLPFLARSFICQMISEAARFOYIEGE 177
Db      139 TAAGKIRENIPGLPALDSAITTLFYNNAN-----SAASALMWLIQSTSEAAKYRFIEQ 193
QY      178 MTRTI 182
Db      194 IGRV 198

RESULT 7
Q41216 PRELIMINARY; PRT; 289 AA.
AC Q41216;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Trichosanthin (EC 3.2.2.22) (rRNA N-glycosidase).
GN TRICHOSANTHIN, TCS.
OS Trichosanthin, kirilowii (Mongolian snake-gourd).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
OX NCBI_TaxID=3677;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94271613; PubMed=8003348;
RA Zheng H., Wang B., Shaw P., Yeung H.;
RT "[Cloning and DNA sequencing of the gene encoding trichosanthin].";
RL I Chuan Hsueh Pao 21:42-51(1994).
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -!- SIMILARITY: BELONGS TO THE 28S RRNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; S70176; AAB31048.1; -
DR HSSP; P09989; 1MRJ.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Hydrolyase; Toxin.
SQ SEQUENCE 289 AA; 31650 MW; 286AC14D48BCA175 CRC64;

Query Match 34.4%; Score 332; DB 10; Length 289;
Best Local Similarity 38.9%; Pred. No. 1.6e-23;
Matches 72; Conservative 42; Mismatches 49; Indels 22; Gaps 5;

QY      9 INFETAGATVQSYTNFIRAVRGLTLPN-----RVGLPINQRFILVLSNHAEL 58
Db      25 VSPRLSGATSSSGVFISNR---KALPNKRLYDIPLLSSLPGSQRYALVHLTYADE 81
QY      59 SVTLALDVTNAYVVGVRAGNSAYFFHPDQEDA-EAITHLFTDVQVRYTFAGNGYDRLE 117
Db      82 TTSVAIDVTNVYMGVRAGDTSYFF---NEASATEAAKVFKDAMRKVTLFPYSGNYERLQ 138
QY      118 QLAGNLRNIELNGPLEEAISALYYSTGQTLPFLARSFICQMISEAARFOYIEGE 177
Db      139 TAAGKIRENIPGLPALDSAITTLFYNNAN-----SAASALMWLIQSTSEAAKYRFIEQ 193
QY      178 MTRTI 182
Db      194 IGRV 198

RESULT 8
O04367 PRELIMINARY; PRT; 563 AA.
AC O04367;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Ribosome inactivating protein precursor (EC 3.2.2.22) (rRNA
DE N-glycosidase).

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OS Sambucus nigra (European elder).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.
OX NCBI_TaxID=4202;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98112023; PubMed=9450339;
RA Van Damme E.J., Roy S., Barre A., Rouge P., Van Leuven F.,
RA Peumans W.J.;
RT "The major elderberry (Sambucus nigra) fruit protein is a lectin
RT derived from a truncated type 2 ribosome-inactivating protein.";
RL Plant J. 12:1251-1260(1997).
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -!- SIMILARITY: BELONGS TO THE 28S RRNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; U76524; AAC15886.1; -
DR HSSP; P02879; 2AAI.
DR InterPro; IPR000772; Ricin_B_lectin.
DR Pfam; PF00652; Ricin_B_lectin; 6.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS00231; RICIN_B_LECTIN; 2.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Hydrolyase; Signal; Toxin.
FT SIGNAL 1 25
FT CHAIN 26 297
FT CHAIN 298 563
FT CHAIN 563 563
SQ SEQUENCE 563 AA; 62336 MW; 3ED2B6C0BE796205 CRC64;

Query Match 34.1%; Score 329.5; DB 10; Length 563;
Best Local Similarity 40.5%; Pred. No. 7e-23;
Matches 77; Conservative 37; Mismatches 51; Indels 25; Gaps 5;

QY      6 YPIINFETAGATVQSYTNFIRAVR-----GRLTVPNRVGLPINQRFILVLSNH 55
Db      28 YPSVSFNLAGAKSATYRDFLKNLRITVATGTVVNGLPVLRRESEVQVKNRFVLLTNY 87
QY      56 AELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAIAI--THLFTDVQVRYTFAGNGY 113
Db      88 NGNTVTTLAVDVTNLYVAVFASANANSYFF-----KDATOLQKSNLFVGR-OHTLPFTGNY 141
QY      114 DLRELQAGNLRNIELNGPLEEAISALYYSTGQTLPFLARSFICQMISEAARFOY 173
Db      142 DNLETAAGTRRESIBLGPSPLDGAITSLYDE-----SVARSLLVVIQMVSEAAARFRI 194
QY      174 IEQEMRTIR 183
Db      195 IEQEVRSRQ 204

RESULT 9
Q9LRE3 PRELIMINARY; PRT; 247 AA.
AC Q9LRE3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Trichobakin (EC 3.2.2.22) (rRNA N-glycosidase) (Fragment).
GN TBK.
OS Trichosanthes sp. Bac Kan 8-98.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
OX NCBI_TaxID=118182;
RN [1]
RP SEQUENCE FROM N.A.
RA Phan Van Chi, Nguyen Thuy Ha, Le Tran Binh;
RT "Genomic DNA clone for mature typ-1 ribosome-inactivating protein from
RT Trichosanthes sp. sample 01 Bac Kan 8-98 Vien CNSH (Hanoi).";
RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

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CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
CC SPECIFIC ADENOSINE ON THE 28S RNA.  
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
DR EMBL; AB039324; BA92530.1; -.  
DR HSP; P09989; IWRJ.  
DR InterPro; IPR001574; RIP.  
DR Pfam; PF00161; RIP; 1.  
DR PRINTS; PR00396; SHIGARICIN.  
DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
KW Hydrolase; Toxin.  
FT NON TER 1 1  
FT 247 247  
SQ SEQUENCE 247 AA; 27199 MW; 89811AC32892F03P CRC64;

Query Match 33.8%; Score 326; DB 10; Length 247;  
Best Local Similarity 39.6%; Pred. No. 4.9e-23;  
Matches 72; Conservative 44; Mismatches 50; Indels 16; Gaps 5;

QY 9 INFTTAGATVQSYTNFIRAVR-----GRLTVLP-NRVGLPINORFILVELSNHAEISVT 61  
Db 2 VSFELSGATSSSYGVFISNLUKALPYERKLDIPILRSTLPFGSORYALIHITNFADETIS 61  
QY 62 LALDVTNAYVGVYRAGNSAYFFHFDNQEADA-EAITHLFTDVQNRYYTFAGGNYDRLEQLA 120  
Db 62 VALDVTNAYVGVYRAGDTSYFF---NEASATEAAKYVFKDAKRVTLPSYSGYERLQIAA 118  
QY 121 GNLRNTELGNGPLEBAISALYYSTGTQPTLARSFIIICIMISAARFOYIEGEMRT 180  
Db 119 GKIRENIPGLPALDSAITTLFFYNAN-----SAASALMVLIOSTSEAAKYKFTQOIGK 173  
QY 181 RI 182  
Db 174 RV 175

RESULT 10  
Q9AVR2 PRELIMINARY; PRT; 564 AA.  
AC Q9AVR2  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Ribosome-inactivating protein precursor (EC 3.2.2.22) (rRNA  
DE N-glycosidase).  
GN EBUL.  
OS Sambucus ebulus.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.  
OX NCBI\_TaxID=28503;  
FN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Leaf;  
RA Gibbs T., Iglesias R., Perez Y., Ferreras J.M., Citores L.;  
RT "Molecular cloning of ebulin 1."  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
CC SPECIFIC ADENOSINE ON THE 28S RNA.  
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
DR EMBL; AJ400822; CAC33178.1; -.  
DR HSP; P02879; 2AAL.  
DR InterPro; IPR000772; Ricin\_B\_lectin.  
DR InterPro; IPR001574; RIP.  
DR Pfam; PF00652; Ricin\_B\_lectin; 6.  
DR Pfam; PF00161; RIP; 1.  
DR PRINTS; PR00396; SHIGARICIN.  
DR SMART; SM00458; RICIN; 2.  
DR PROSITE; PS00231; RICIN B LECTIN; 2.  
DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
KW Glycosidase; Hydrolase; Signal; Toxin.  
FT SIGNAL 1 25 POTENTIAL.  
FT CHAIN 26 298 EBULIN L A-CHAIN.  
FT CHAIN 299 564 EBULIN L B-CHAIN.

SQ SEQUENCE 564 AA; 62694 MW; 8261681A6DB55CB8 CRC64;  
Query Match 33.5%; Score 323.5; DB 10; Length 564;  
Best Local Similarity 40.0%; Pred. No. 2.6e-22;  
Matches 76; Conservative 38; Mismatches 51; Indels 25; Gaps 6;

QY 6 YPLIINFTTAGATVQSYTNFIRAVRG-----LTVLPRVGLPINORFILVELSNH 55  
Db 28 YPSVSENLGAKSTTYRDFLKNLRDRAVATGYEVNGLPVLRRSEVGVQKRFVLVRITNY 87  
QY 56 AELSVTLALDVTNAYVGVYRAGNSAYFFHFDNQEADAEL--THLFTDVQNRYYTFAGGNY 113  
Db 88 NGDTVTSADVDTNLYLVAFSANGSYFF-----KDATLQKSNLFGT-TQHTLSFTGNY 141  
QY 114 DRLEQLAGNIRENIELGNGPLEBAISALYYSTGTQPTLARSFIIICIMISAARFOY 173  
Db 142 DNLETAAGTRRESIELGPNFLDGAITSWY--DGG-----VARSLVLIQVMPFAARFY 194  
QY 174 IEGEMRTIR 183  
Db 195 IEQEVRRSLQ 204

RESULT 11  
Q06076 PRELIMINARY; PRT; 528 AA.  
ID Q06076  
AC Q06076  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Abrin-d (EC 3.2.2.22) (rRNA N-glycosidase) (Fragment).  
DE Abrus precatorius (Indian licorice) (Crab's eye).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.  
OX NCBI\_TaxID=3816;  
FN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=93132798; PubMed=8421313;  
RX Hung C.-H., Lee M.-C., Lee T.-C., Lin J.-Y.;  
RT "Primary structure of three distinct isoabrin determined by cDNA  
RT sequencing: conservation and significance."  
RL J. Mol. Biol. 229:263-267(1993).  
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
CC SPECIFIC ADENOSINE ON THE 28S RNA.  
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
DR EMBL; M98346; AAA32626.1; -.  
DR HSP; P11140; IABR.  
DR InterPro; IPR000772; Ricin\_B\_lectin.  
DR InterPro; IPR001574; RIP.  
DR Pfam; PF00652; Ricin\_B\_lectin; 6.  
DR Pfam; PF00161; RIP; 1.  
DR PRINTS; PR00396; SHIGARICIN.  
DR SMART; SM00458; RICIN; 2.  
DR PROSITE; PS00231; RICIN B LECTIN; 2.  
DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
KW Hydrolase; Toxin.  
FT NON TER 1 1  
FT NON TER 528 528  
SQ SEQUENCE 528 AA; 58870 MW; 62ED42FB8FF60F8 CRC64;

Query Match 33.0%; Score 318.5; DB 10; Length 528;  
Best Local Similarity 43.3%; Pred. No. 7.2e-22;  
Matches 81; Conservative 22; Mismatches 69; Indels 15; Gaps 4;

QY 5 QYPIINFTTAGATVQSYTNFIRAVRGELT-----VLNPRVGLPINORFILVELSNHA 56  
Db 1 QDQVIKFTTEGATSSQYKQFIEALRQLTHIDIPVLDPPTVEERNRYITVELSNSE 60  
QY 57 ELSVTLALDVTNAYVGVYRAGNSAYFFHFDNQEADAELTHLFTDVQNRYYTFAGGNYDR 116  
Db 61 RESIEVGIDVTNAYVWAYRAGSQSYFL---RDAPASASTYLFPGTQ-RYSLRFDGSGYDL 116

OS *Abrus precatorius* (Indian licorice) (Crab's eye).  
OC *Eukaryota*; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC *Spermatophyta*; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC *eucosids I*; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.  
NCBI\_TaxID=3816;  
[1]  
RN SEQUENCE FROM N.A.  
RP  
RC TISSUE=LEAF;  
RX MEDLINE=91201329; PubMed=2016300;  
RA Evensen G., Mathiesen A., Sundan A.;  
RT "Direct molecular cloning and expression of two distinct abrin A-  
chains.";  
RL J. Biol. Chem. 266:6848-6852(1991).  
CC -!- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN  
CC SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL  
CC SUBUNIT BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA.  
CC ABRIN-A IS MORE TOXIC THAN RICIN.  
CC -!- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT  
CC FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT  
CC PRECEDES ENDOCYTOSIS.  
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
CC SPECIFIC ADENOSINE ON THE 28S RNA.  
CC -!- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.  
CC -!- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN  
CC CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).  
CC -!- SIMILARITY: TO OTHER BACTERIAL AND PLANTS RIBOSOME-INACTIVATING  
CC PROTEINS. BELONGS TO TYPE 2 RIP.  
CC EMBL; X54872; CAA38654.1; --  
CC HSSP; P11140; 1ABR.  
DR InterPro; IPR001574; RIP.  
DR Pfam; PF00161; RIP; 1.  
DR PRINTS; PR00396; SHIGARICIN.  
DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
KW Hydrolase; Glycosidase; Toxin; Repeat; Glycoprotein; Lectin.  
FT CHAIN 1 252 ABRIN E, A CHAIN (BY SIMILARITY).  
FT NON\_TER 252 252  
SQ SEQUENCE 252 AA; 28309 MW; BBFC846B9E92B85DE CRC64;  
Query Match 32.2%; Score 310.5; DB 10; Length 252;  
Best Local Similarity 43.2%; Pred. No. 1.5e-21;  
Matches 79; Conservative 22; Mismatches 67; Indels 15; Gaps 4;  
QY 9 INETTAGVQSVNTNIRAVRGL-----TVLPNRVLGPINQRFILVELSHAELSV 60  
Db 6 IKFSTEGATQSQYKQFIEALRELRGLIHDIPLVRDPTTVEENRYITVELSNSRESI 65  
QY 61 TLALDVNAVVGVRAGNSAYFFHPDNOEAAETHLFTDVQNRYTEAFGNGYRLEOLA 120  
Db 66 EVCIDVNAVVAVRAGSQSYFL--RDAPASASTYLTGTQ-RYSLRFDSYGDLEKWA 121  
QY 121 GNLRNIEIENGPLERAISALYYVTGTGTPLTARSFFICIMISPAARQYTEGMRT 180  
Db 122 HQTRQETISGLQALTHAIS---FLRSGASNDKARTLVIIOQASAAARYVISNRVGV 178  
QY 181 RIR 183  
Db 179 SIR 181  
RESULT 14  
Q945S2  
ID Q945S2 PRELIMINARY; PRT; 563 AA.  
AC Q945S2;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Ribosome-inactivating protein (EC 3.2.2.22) (tRNA  
DE N-glycosidase).  
GN AVL.  
OS *Sambucus nigra* (European elder).  
OC *Eukaryota*; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC *Spermatophyta*; Magnoliophyta; eudicotyledons; core eudicots;  
OC *Asteridae*; campanulids; Dipsacales; Adoxaceae; Sambucus.

OX NCBI\_TaxID=4202;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Leaf;  
 RA van Damme E.J.M.;  
 RT "Characterization and cloning of lectins and ribosome-inactivating  
 RL proteins from *Sambucus nigra* leaves."  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 CC SPECIFIC ADENOSINE ON THE 28S RNA.  
 CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 DR EMBL; AF409135; AAL04123.1; -  
 DR InterPro; IPR000772; Ricin\_B\_lectin.  
 DR InterPro; IPR001574; RIP.  
 DR Pfam; PF00652; Ricin\_B\_lectin; 6.  
 DR Pfam; PF00161; RIP; 1.  
 DR PRINTS; PR00396; SHIGARICIN.  
 DR SMART; SM00458; RICIN; 2.  
 DR PROSITE; PS02031; RICIN\_B\_LECTIN; 2.  
 DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
 KW Hydrolase; Toxin.  
 SQ SEQUENCE 563 AA; 62242 MW; 07F7CBEDCF33BF10 CRC64;

Query Match 31.9%; Score 307.5; DB 10; Length 563;  
 Best Local Similarity 38.4%; Pred. NO. 8.9e-21;  
 Matches 73; Conservative 36; Mismatches 56; Indels 25; Gaps 5;  
 QY 6 YPIINFITAGATVQSYTNFIRAVR-----GRLTVPNRYGLPINORFILVELSNH 55  
 DB 28 YPSVSFNLGAKSATYRDFLSNLRKTVATGTYEVNGLPVLRRESEVQVKSFRVLPLTNY 87  
 QY 56 AELSVTLALDVNTNAYVVGVRAGNSAYFFHPDNOEDAEAI--THLFTDVQNRYYTFAFGNY 113  
 DB 88 NGNTVTTLAVDVNTNLYVAVFGNSANSYFF-----KDATEVQKSNLFVGTQKQ-TLSFTGNY 141  
 QY 114 DRLEQLAGNLRNLELNGPLERALSALYYSTGTQPTLARSFIICIMISEARFOY 173  
 DB 142 DNLETAANTRESIEELGSPDLGATISLYHGD-----SVARSLLVVIQMVSEARFRY 194  
 QY 174 IEGERMTRIR 183  
 DB 195 IEQEVRESLQ 204

RESULT 15  
 Q8GT32 PRELIMINARY; PRT; 563 AA.  
 AC Q8GT32;  
 DT 01-MAR-2003 (TREMELrel. 23, Created)  
 DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)  
 DE Type 2 ribosome-inactivating protein nigrin 1 precursor  
 DE (EC 3.2.2.22).  
 OS *Sambucus nigra* (European elder).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.  
 OX NCBI\_TaxID=4202;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Leaf;  
 RA Gibbs T., Arias F.J., Antolin P.;  
 RT "Characterization and molecular cloning of Nigrin 1, a type two  
 RL ribosome-inactivating protein from leaves of elder (*Sambucus nigra*)."  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF249280; AAN86130.1; -  
 KW Hydrolase; Glycosidase.  
 SQ SEQUENCE 563 AA; 62173 MW; 0EB236421FC5R04F CRC64;

Query Match 31.9%; Score 307.5; DB 10; Length 563;  
 Best Local Similarity 38.4%; Pred. NO. 8.9e-21;  
 Matches 73; Conservative 36; Mismatches 56; Indels 25; Gaps 5;

QY 6 YPIINFITAGATVQSYTNFIRAVR-----GRLTVPNRYGLPINORFILVELSNH 55  
 DB 28 YPSVSFNLGAKSATYRDFLSNLRKTVATGTYEVNGLPVLRRESEVQVKSFRVLPLTNY 87  
 QY 56 AELSVTLALDVNTNAYVVGVRAGNSAYFFHPDNOEDAEAI--THLFTDVQNRYYTFAFGNY 113  
 DB 88 NGNTVTTLAVDVNTNLYVAVFGNSANSYFF-----KDATEVQKSNLFVGTQKQ-TLSFTGNY 141  
 QY 114 DRLEQLAGNLRNLELNGPLERALSALYYSTGTQPTLARSFIICIMISEARFOY 173  
 DB 142 DNLETAANTRESIEELGSPDLGATISLYHGD-----SVARSLLVVIQMVSEARFRY 194  
 QY 174 IEGERMTRIR 183  
 DB 195 IEQEVRESLQ 204

Search completed: February 10, 2004, 16:26:38  
 Job time : 25.0852 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:13:20 ; Search time 31.5419 Seconds  
(without alignments)  
930.966 Million cell updates/sec

Title: US-10-083-336A-9

Perfect score: 951

Sequence: 1 IPFKQYPIINFITAGATQVS.....ARFQYIEGEMTRIRYNRS 185

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_19Jun03:\*

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2:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
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18:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
19:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
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23:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	934.5	98.3	267	14	AAR37290 Ricin A chain. Un
2	934.5	98.3	267	16	AAR37290 Ricin A-chain (RTA
3	934.5	98.3	290	18	AAW25136 Ricin A-chain ribo
4	934.5	98.3	290	18	AAW21699 Ricin A-chain RIP.
5	934.5	98.3	332	8	AAP70097 Ricin A. Escheric
6	934.5	98.3	332	8	AAP70097 Ricin A. Escheric
7	934.5	98.3	332	10	AAP5639 Sequence of Ricinu
8	934.5	98.3	554	16	AAR70827 Ricin A encoded by
9	934.5	98.3	562	10	AAP90079 Anti-catact immu
					Ricin D. Ricinus

10	934.5	98.3	565	6	AAP50166 Sequence of prepro
11	934.5	98.3	565	22	AAG78300 Castor bean prepro
12	934.5	98.3	565	22	AAG78300 Modified castor be
13	934.5	98.3	576	8	AAP70326 Sequence of Ricinu
14	934.5	98.3	576	18	AAW25787 Castor bean ricin.
15	934.5	98.3	576	20	AAV58992 Castor bean ricin
16	934.5	98.3	576	21	AAV78592 Ricinus communis r
17	934.5	98.3	576	22	AAG78301 Castor bean prepro
18	934.5	98.3	576	22	AAG78302 Castor bean prepro
19	930.5	97.8	200	9	AAP80164 Biosynthetic multi
20	929.5	97.7	565	7	AAP60240 Preproricin. Ricin
21	927.5	97.5	268	14	AAR39570 Sequence of Ricinu
22	927.5	97.5	574	8	AAP70325 DNA sequence of ri
23	925.5	97.3	574	10	AAP94793 Ricin A from PIC11
24	924.5	97.2	267	13	AAR30722 Amino acid sequenc
25	924.5	97.2	267	21	AAW19265 Sequence of G-FIT.
26	924.5	97.2	534	14	AAR39571 Ricin A gene produ
27	923.5	97.1	332	11	AAR06554 Ricin A chain (RTA
28	917.5	96.5	267	16	AAR74176 Ricin A. Syntheti
29	901.5	94.8	267	14	AAR32430 Castor oil plant a
30	845	88.9	540	18	AAW25143 R. communis agglut
31	845	88.9	540	18	AAW21706 Sequence of Ricin
32	803	84.4	534	8	AAP70324 Ricin agglutinin A
33	698	73.4	280	10	AAP95648 Trichosanthin anti
34	337.5	35.5	247	16	AAR67359 Amino acid sequenc
35	337.5	35.5	247	21	AAV69048 Synthetic alpha-tr
36	337.5	35.5	248	11	AAR07518 Mature alpha-Trich
37	337.5	35.5	248	13	AAR25573 Trichosanthin (a r
38	337.5	35.5	267	18	AAW25140 Trichosanthin. Tr
39	337.5	35.5	267	18	AAW21703 Trichosanthin from
40	337.5	35.5	289	11	AAR07514 Trichosanthin from
41	337.5	35.5	289	13	AAR25572 Trichosanthin prot
42	337.5	35.5	289	13	AAR29272 Trichosanthin chine
43	337.5	35.5	289	14	AAR32986 Encodes chinese cu
44	337.5	35.5	289	15	AAR55129 Alpha-trichosanthi
45	337.5	35.5	289	18	AAW10468 Chinese cucumber a

## ALIGNMENTS

### RESULT 1

AAR37290  
ID AAR37290 standard; protein; 267 AA.

XX AAR37290;

AC AAR37290;

XX AAR37290;

XX AAR37290;

XX AAR37290;

XX AAR37290;

XX AAR37290;

XX AAR37290;

XX AAR37290;

XX AAR37290;

XX AAR37290;

XX AAR37290;

XX AAR37290;

XX AAR37290;

XX AAR37290;

XX AAR37290;

XX AAR37290;

XX AAR37290;

XX AAR37290;

XX AAR37290;

XX AAR37290;

XX AAR37290;

XX AAR37290;

XX AAR37290;

XX AAR37290;

XX AAR37290;

XX AAR37290;

XX AAR37290;

XX AAR37290;

XX AAR37290;

XX AAR37290;

XX AAR37290;

XX AAR37290;

PT Analogues of type I ribosome inactivating protein - useful as  
PT cytotoxic agents, immuno toxins for treating auto immune diseases,  
PT cancer, graft versus host disease and selective cell killing in-vivo  
XX  
XX  
XX Claim 1; Page 92; 163pp; English.  
XX  
XX The invention covers analogues of Type I RIPS. Ricin is a Type II  
CC RIP whose A chain is homologous to plant type I RIPS. The analogues  
CC of the invention have a cysteine available for intermolecular  
CC disulphide bonding at an amino acid position corresp. to a position  
CC not naturally available for bonding; the cys residue is located in  
CC the C-terminal region of the analogue between a position corresp. to  
CC amino acid 251 and the C-terminus of ricin A chain. The analogues are  
CC pref. joined via a disulphide linkage to a molecule which specifically  
CC binds to a target cell, e.g. an antibody fragment.  
CC (Updated on 09-JAN-2003 to add missing OS field.)  
XX  
XX (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 267 AA;  
Query Match 98.3%; Score 934.5; DB 14; Length 267;  
Best Local Similarity 93.4%; Pred. No. 2.3e-91;  
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;  
QY 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINORFILV 47  
DB 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTGADVHEIPVLPNRVGLPINORFILV 60  
QY 48 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHTLFTDVQNYRTFAFG 107  
DB 61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHTLFTDVQNYRTFAFG 120  
QY 108 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIQIMISEAAR 167  
DB 121 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIQIMISEAAR 180  
QY 168 FOYIEGEMTRIRYNRRS 185  
DB 181 FOYIEGEMTRIRYNRRS 198  
RESULT 2  
AAR63902  
ID AAR63902 standard; protein; 267 AA.  
XX  
XX AAR63902;  
XX  
XX 25-MAR-2003 (updated)  
DT 27-JUL-1995 (first entry)  
XX  
XX Ricin A-chain (RTA).  
XX Ricin A chain; RTA; ribosome-inactivating proteins; RIPS;  
KW cytotoxic therapeutic agents; autoimmune disease; cancer;  
KW graft-versus-host disease.  
XX  
XX Ricinus communis.  
XX  
XX WO9426910-A1.  
XX  
XX 24-NOV-1994.  
XX  
XX 12-MAY-1994; 94WO-US05348.  
XX  
XX 12-MAY-1993; 93US-0064691.  
XX  
XX (XOMA ) XOMA CORP.  
XX  
XX Better MD, Carroll SS, Studnicka GM, Carroll SF;  
XX  
XX WPI; 1995-006804/01.  
XX  
XX Polynucleotide(s) encoding type I ribosome-inactivating proteins  
PT

PT - which are suitable for use as components of cytotoxic  
PT therapeutic agents.  
XX  
XX Example 3; Fig 1; 221pp; English.  
XX  
XX AAR63902 is the ricin A chain gene product, it is analogous to the  
CC ribosome-inactivating proteins (RIPs) described in AAR63903-R63911.  
CC RIPs are the key components of cytotoxic therapeutic agents (CTAs),  
CC which include gene fusion products and immunoconjugates. CTAs may  
CC be used to selectively eliminate any cell type to which a RIP  
CC component is targeted, by the specific binding capacity of the  
CC second component of the agent. They can be used in the treatment  
CC of diseases where the elimination of a particular cell type is  
CC desired, such as autoimmune disease, cancer and graft-versus-host  
CC disease.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
XX Sequence 267 AA;  
SQ  
Query Match 98.3%; Score 934.5; DB 16; Length 267;  
Best Local Similarity 93.4%; Pred. No. 2.3e-91;  
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;  
QY 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINORFILV 47  
DB 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTGADVHEIPVLPNRVGLPINORFILV 60  
QY 48 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHTLFTDVQNYRTFAFG 107  
DB 61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHTLFTDVQNYRTFAFG 120  
QY 108 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIQIMISEAAR 167  
DB 121 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIQIMISEAAR 180  
QY 168 FOYIEGEMTRIRYNRRS 185  
DB 181 FOYIEGEMTRIRYNRRS 198  
RESULT 3  
AAW25136  
ID AAW25136 standard; Protein; 290 AA.  
XX  
XX AAW25136;  
XX  
XX 25-MAR-2003 (updated)  
DT 02-DEC-1997 (first entry)  
XX  
XX Ricin A-chain ribosome inhibitory protein inactive precursor.  
XX  
XX Maize; proRIP; ribosome inactivating protein; alpha; beta subunit;  
KW internal linker; Barley Translation inhibitor; Trichosanthin;  
KW Ricin A-chain; Abrin-A chain; Saporin; SLT-1; Luffin A; MAP;  
KW Ricinus communis agglutinin; Momordin; PAP-S; Luffin-B; Dianthin 30;  
KW therapeutic toxin; tumour cell targeted; protein synthesis inhibitor;  
KW post-translational modification; cancer; neoplasia; HIV; AIDS;  
KW human immunodeficiency virus; acquired immune deficiency syndrome.  
XX  
XX Synthetic.  
XX  
XX US5646026-A.  
XX  
XX 08-JUL-1997.  
XX  
XX 07-JUN-1995; 95US-0485286.  
XX  
XX 09-DEC-1992; 92US-0987927.  
XX  
XX 11-JUN-1990; 90US-0535636.  
XX  
XX 26-JAN-1995; 95US-0378761.  
XX  
XX 07-JUN-1995; 95US-0485286.  
XX  
XX (DOWC ) DOWELANCO.  
PA

XX PI Hey TD, Morgan AER, Walsh TA;  
 XX DR WPI; 1997-362934/33.  
 XX  
 XX DNA encoding pro-ribosome inactivating proteins - inactive  
 PT precursors of ribosome inactivating proteins; can be expressed in  
 PT eukaryotic cells without causing cell death  
 XX  
 XX Claim 4; Column 91-94; 186pp; English.  
 PS  
 XX AAW215136 represents a Ricin A-chain ribosome inhibitory protein (RIP)  
 CC which was engineered to contain a selectively removable internal peptide  
 CC linker sequence separating the alpha and beta units of the RIP. When  
 CC separated the two units regain activity and are capable of inactivating  
 CC eukaryotic ribosomes and hence preventing protein production. Many  
 CC different RIPs may be produced with an internal linker including  
 CC maize RIP, Trichosanthin, Ricin A-chain, Abrin-A A-chain and  
 CC Saporin. The RIPs can be used in the construction of therapeutic  
 CC toxins targeted to specific cells such as tumour cells via the  
 CC attachment of a targeting polypeptide, e.g. a monoclonal antibody.  
 CC A further use is in HIV therapy (see US4869903). There is interest  
 CC in expressing RIP recombinantly in host eukaryotic cells, because of  
 CC the capacity to provide correct post-translational processing. However,  
 CC RIPs effectively inhibit protein synthesis in eukaryotic cells resulting  
 CC in cell death. Since the inactive RIP proteins are not cytotoxic to  
 CC eukaryotic cells, they can be recombinantly expressed in such cells and  
 CC then converted to active RIP proteins.  
 CC (Updated on 25-MAR-2003 to correct PF field.)  
 XX  
 XX Sequence 290 AA;  
 SQ  
 Query Match 98.3%; Score 934.5; DB 18; Length 290;  
 Best Local Similarity 93.4%; Pred. No. 2.5e-91;  
 Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;  
 QY 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGLT-----NRVGLPINQRFILV 47  
 DB 25 IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTGDVRRHEIPVLPNRVGLPINQRFILV 84  
 QY 48 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 107  
 DB 85 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 144  
 QY 108 GNYDRLEQLAGNLRNIELNGPLEEAI SALLYSTGGTQLPRLARSFIIICIMISEAR 167  
 DB 145 GNYDRLEQLAGNLRNIELNGPLEEAI SALLYSTGGTQLPRLARSFIIICIMISEAR 204  
 QY 168 FOYIEGEMTRIRYNRRS 185  
 DB 205 FOYIEGEMTRIRYNRRS 222  
 RESULT 4  
 AAW21699  
 ID AAW21699 standard; Protein; 290 AA.  
 XX AC AAW21699;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 26-SEP-1997 (first entry)  
 XX Ricin A-chain RIP.  
 XX  
 KW pro-Ribosome Inactivating Protein; proRIP; peptide linker; cancer;  
 KW inactivation; eukaryotic ribosome; alpha fragment; beta fragment;  
 KW inhibitor; protein synthesis; N-glycosidase; glycosidic bond; liver;  
 KW rat; ribosomal 28S RNA; cellular proliferation; HIV-infected T cell.  
 XX Ricinus communis.  
 XX Key Location/Qualifiers  
 FH Region 152..162  
 FT

FT  
 FT  
 XX  
 XX US5635384-A.  
 XX  
 XX 03-JUN-1997.  
 XX  
 XX 26-JAN-1995; 95US-0378761.  
 XX  
 XX 09-DEC-1992; 92US-0987927.  
 XX 11-JUN-1990; 90US-0535636.  
 XX 26-JAN-1995; 95US-0378761.  
 XX (DOWC ) DOWELANCO.  
 XX Hey TD, Morgan AER, Walsh TA;  
 XX WPI; 1997-309831/28.  
 XX  
 XX Inactive precursor of maize ribosome-inactivating protein - also  
 PT chimeric ribosome-inactivating protein precursors containing  
 PT internal linker sequences  
 XX  
 XX Claim 2; Column 91-94; 121pp; English.  
 XX  
 XX The sequences given in AAW21698-710 represent Ribosome Inactivating  
 CC proteins (RIP's), which may be used in the construction of the  
 CC proRIP of the invention. The proRIP has a selectively removable,  
 CC internal peptide linker. The precursor sequence is incapable of  
 CC inactivating eukaryotic ribosomes, but can be converted by removal  
 CC of the linker into a protein having alpha and beta fragments and being  
 CC capable of inactivating eukaryotic ribosomes. RIPs are potent  
 CC inhibitors of eukaryotic protein synthesis. They possess a highly  
 CC specific N-glycosidase activity which cleaves the glycosidic bond of  
 CC adenine 4324 of rat liver ribosomal 28S RNA. RIP's selectively inhibit  
 CC cellular proliferation of cells, e.g. cancer cells and HIV-infected T  
 CC cells. The inactive proRIP proteins make it possible to provide protein  
 CC synthesis inhibitors with uses in practical and improved ways not before  
 CC possible. The RIP can be used to make cytotoxic conjugates.  
 CC (Updated on 25-MAR-2003 to correct PF field.)  
 XX  
 XX Sequence 290 AA;  
 SQ  
 Query Match 98.3%; Score 934.5; DB 18; Length 290;  
 Best Local Similarity 93.4%; Pred. No. 2.5e-91;  
 Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;  
 QY 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGLT-----NRVGLPINQRFILV 47  
 DB 25 IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTGDVRRHEIPVLPNRVGLPINQRFILV 84  
 QY 48 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 107  
 DB 85 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 144  
 QY 108 GNYDRLEQLAGNLRNIELNGPLEEAI SALLYSTGGTQLPRLARSFIIICIMISEAR 167  
 DB 145 GNYDRLEQLAGNLRNIELNGPLEEAI SALLYSTGGTQLPRLARSFIIICIMISEAR 204  
 QY 168 FOYIEGEMTRIRYNRRS 185  
 DB 205 FOYIEGEMTRIRYNRRS 222  
 RESULT 5  
 AAW70037  
 ID AAW70037 standard; protein; 332 AA.  
 XX AC AAW70037;  
 XX  
 DT 09-APR-1991 (first entry)  
 XX Ricin A.  
 DE

/note= "Position of possible insertion of internal  
 peptide linker sequence"

XX Ricin A; Met-aminopeptidase.  
 KW Escherichia coli.  
 OS  
 XX EP219237-A.  
 XX  
 XX 22-APR-1987.  
 PD  
 XX 19-SEP-1986; 86EP-0307242.  
 PF  
 XX 06-MAY-1986; 86US-0860330.  
 XX  
 PR 20-SEP-1985; 85US-0778414.  
 XX  
 XX (CETU ) CETUS CORP.  
 PA  
 XX Benbassat A, Bauer KA, Chang S, Chang SY;  
 PI  
 XX WPI; 1987-110172/16.  
 DR  
 DR N-PSDB; AAN70152.  
 XX  
 XX N-terminal methionine free proteins prodn. - by using host  
 PT transformed with vector to express a methionine-amino-peptidase  
 PT  
 XX Disclosure; Fig. 4; 20pp; English.  
 PS  
 XX Ricin A may be produced in a form which lacks an N-terminal Met  
 CC using Met-aminopeptidase from E.coli.  
 CC  
 XX Sequence 332 AA;  
 SQ  
 Query Match 98.3%; Score 934.5; DB 8; Length 332;  
 Best Local Similarity 93.4%; Pred. No. 3e-91;  
 Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;  
 QY 1 IFFKQYPIINFETAGATVQSYTNFIRAVRGLT-----NRVGLPINQRFILV 47  
 Db 36 IFFKQYPIINFETAGATVQSYTNFIRAVRGLTTGADVVRHEIPVLPNRVGLPINQRFILV 95  
 QY 48 ELSNHAELSVTLALDVTNAYVGYRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAFG 107  
 Db 96 ELSNHAELSVTLALDVTNAYVGYRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAFG 155  
 QY 108 GNYDRLEQLAGNLRENIELGNGLPELEAISALYYSTGGTQPLTLARSFIIQIMISEAAR 167  
 Db 156 GNYDRLEQLAGNLRENIELGNGLPELEAISALYYSTGGTQPLTLARSFIIQIMISEAAR 215  
 QY 168 FOYIEGEMTRIRYNRRS 185  
 Db 216 FOYIEGEMTRIRYNRRS 233  
 RESULT 6  
 AAP70838  
 ID AAP70838 standard; protein; 332 AA.  
 XX  
 XX AAP70838;  
 AC  
 XX 25-MAR-2003 (updated)  
 DT 18-FEB-1991 (first entry)  
 XX  
 XX Sequence of Ricinus communis castor beans ricin toxin (RT or ricin)  
 DE A protein encoded by pRA123.  
 DE  
 XX Lectin; toxin protein; cytotoxic; castor bean;  
 KW plant toxin.  
 KW  
 XX Ricinus communis.  
 OS  
 XX Key Location/Qualifiers  
 FH 1..32  
 FT Region /note="Leader"  
 FT 33..302  
 FT

FT Region /note="A-chain"  
 FT 315..332  
 FT /note="B-chain"  
 XX  
 XX EP237676-A.  
 XX  
 XX 23-SEP-1987.  
 PD  
 XX 13-NOV-1986; 86EP-0308877.  
 PF  
 XX 07-MAR-1986; 86US-0837583.  
 PR  
 XX (CETU ) CETUS CORP.  
 PA  
 PA (CHIR ) CHIRON CORP.  
 XX  
 XX Piatak M;  
 PI  
 XX WPI; 1987-265177/38.  
 DR  
 DR N-PSDB; AAN70519.  
 XX  
 XX New non-glycosylated ricin precursor and toxin etc. - are prepd.  
 PT by recombinant DNA procedures with specific isolation steps for  
 PT purer and soluble prods.  
 PT  
 XX Disclosure; Fig 1; 112pp; English.  
 PS  
 XX The full-length sequences encoding ricin A (AAN70520), ricin D  
 CC (AAN70525), putative ricin B (AAN70526) and RCA (AAN70524) in precursor  
 CC form were obtd. using messenger RNA to obtain a cDNA library, and  
 CC then probing the library to retrieve the desired cDNA inserts. The  
 CC library was probed using the 35-mer given in AAN70514. Figure 4 (see  
 CC AAN70520, AAN70521, AAN70522) shows the nucleotide sequences of three  
 CC plasmids contg. cDNA inserts obtd. by probing a cDNA library for  
 CC sequences encoding ricin B using the probe in AAN70517. The cDNA  
 CC inserts can be placed into expression vectors. Site-directed  
 CC mutagenesis may be used to place an ATG start codon and a HindIII  
 CC site at the beginning of the mature protein (see AAN70518). The  
 CC coding sequences of the inserts can be ligated into expression  
 CC vectors contg. the Phoa promoter-operator and leader sequence  
 CC (AAN70523) and suitable retroregulators.  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 332 AA;  
 Query Match 98.3%; Score 934.5; DB 8; Length 332;  
 Best Local Similarity 93.4%; Pred. No. 3e-91;  
 Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;  
 QY 1 IFFKQYPIINFETAGATVQSYTNFIRAVRGLT-----NRVGLPINQRFILV 47  
 Db 36 IFFKQYPIINFETAGATVQSYTNFIRAVRGLTTGADVVRHEIPVLPNRVGLPINQRFILV 95  
 QY 48 ELSNHAELSVTLALDVTNAYVGYRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAFG 107  
 Db 96 ELSNHAELSVTLALDVTNAYVGYRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAFG 155  
 QY 108 GNYDRLEQLAGNLRENIELGNGLPELEAISALYYSTGGTQPLTLARSFIIQIMISEAAR 167  
 Db 156 GNYDRLEQLAGNLRENIELGNGLPELEAISALYYSTGGTQPLTLARSFIIQIMISEAAR 215  
 QY 168 FOYIEGEMTRIRYNRRS 185  
 Db 216 FOYIEGEMTRIRYNRRS 233  
 RESULT 7  
 AAP95639  
 ID AAP95639 standard; protein; 332 AA.  
 XX  
 XX AAP95639;  
 AC  
 XX 25-MAR-2003 (updated)  
 DT 31-OCT-2002 (updated)  
 DT

DT 13-AUG-1990 (first entry)  
XX Ricin A encoded by insert from plasmid pRA123.  
XX Plasmid pRA123; ricin-A; ricin-B; cytotoxicity.  
XX Ricinus communis.  
OS Synthetic.  
XX Key Location/Qualifiers  
FT 1..35 /label= leader sequence  
FT Peptide 36..302 /label=A-chain  
FT Peptide 303..314 /label=linker  
FT Peptide 315..332 /label=B-chain  
FT EP335476-A.  
FN 04-OCT-1989.  
XX 19-JAN-1989; 89EP-0201162.  
XX 08-FEB-1984; 84US-0578115.  
XX 08-FEB-1984; 84US-0578121.  
XX 09-FEB-1984; 84US-0578122.  
XX 07-SEP-1984; 84US-0648759.  
XX 20-SEP-1984; 84US-0653515.  
XX (CETU) CETUS CORPORATION.  
XX Gelfand D, Lawyer PC, Horn G, Greenfield L, Nitecki D, Kaplan D;  
PI Platak MJ;  
XX WP7; 1989-286959/40.  
XX N-PSDB; AAN91281.  
XX Recombinant vectors expressing ricin chains or diphtheria toxin -used for  
PT prodn. of new immunotoxin conjugates with monoclonal antibodies, having  
PT high cell specificity and good extracellular stability.  
XX Disclosure; Fig 14; 54pp; English.  
XX Plasmid RA123 (ATCC No. 39799) carries the entire coding sequence for  
CC ricin A, as well as codons for 12 AAs joining the A to the B chain.  
CC Following modification for ease of manipulation the plasmid was used to  
CC construct expression vectors which express the conjugates in  
CC host cells.  
CC (Updated on 31-OCT-2002 to add missing OS field.)  
CC (Updated on 25-MAR-2003 to correct PF field.)  
CC (Updated on 25-MAR-2003 to correct PR field.)  
CC (Updated on 25-MAR-2003 to correct PI field.)  
XX SQ Sequence 332 AA;  
Query Match 98.3%; Score 934.5; DB 10; Length 332;  
Best Local Similarity 93.4%; Pred. No. 3e-91; Indels 13; Gaps 1;  
Matches 185; Conservative 0; Mismatches 0;  
QY 1 IPPKQYPIINFATTAGATVQSYTNFIRAVRGRLT-----NRVGLPINQRFILV 47  
DB 36 IPPKQYPIINFATTAGATVQSYTNFIRAVRGRLTTCGADVREHETPVLNVRVGLPINQRFILV 95  
QY 48 ELSNHAELSVTIALDVNTAYVGVYRAGNSAYFFHPDNDQEDAEAIHTLFTDVQNRVTFAPG 107  
DB 96 ELSNHAELSVTIALDVNTAYVGVYRAGNSAYFFHPDNDQEDAEAIHTLFTDVQNRVTFAPG 155  
QY 108 GNYDRLEQAGNLRENIELNGPLBEASALYYVYGGTQGLPTLARSFICIQMISEAR 167  
DB 156 GNYDRLEQAGNLRENIELNGPLBEASALYYVYGGTQGLPTLARSFICIQMISEAR 215

QY 168 FOYIEGEMRTRIRYNRRS 185  
DB 216 FOYIEGEMRTRIRYNRRS 233  
RESULT 8  
AAR70827  
ID AAR70827 standard; Protein; 554 AA.  
XX AAR70827;  
AC AAR70827;  
XX 25-MAR-2003 (updated)  
DT 31-AUG-1995 (first entry)  
XX Anti-cataract immunotoxin.  
XX Immunotoxin; heavy chain; light chain; variable region; antibody;  
KW ricin-A; cytostatic; cataract; lens opacification; epithelial cell;  
KW pHB19; 4197X; monoclonal antibody; MAb.  
XX Synthetic.  
XX Key Location/Qualifiers  
FT 1..27 /label= Sig\_peptide  
FT Peptide /note= "phoA signal sequence"  
FT Domain 28..145 /label= HEAVY  
FT Peptide /note= "MAb 4197X heavy chain"  
FT Peptide 148..166 /label= LINKER  
FT Domain 169..274 /label= LIGHT  
FT Peptide /note= "MAb 419X light chain"  
FT Domain 276..544 /label= RICIN-A  
FT Peptide 549..554 /label= TAG  
FT Peptide /note= "hexa-histidine tail"  
XX WO9503828-A1.  
XX 09-FEB-1995.  
XX 15-JUL-1994; 94WO-US07919.  
XX 02-AUG-1993; 93US-0101329.  
XX (HOUS-) HOUSTON BIOTECHNOLOGY INC.  
XX Gould RM, Kelleher PJ, Wallace TL, Wood MS;  
XX WPI; 1995-082036/11.  
XX N-PSDB; AAQ85386.  
XX New single chain immuno:toxin - binds specifically to epithelial  
PT cells, for inhibiting development of sec. cataracts after  
PT extra:capsular cataract extraction.  
XX Disclosure; Fig.4; 68pp; English.  
XX The immunotoxin given in AAR70827 comprises the heavy and light chain  
CC variable regions of anti-lens epithelium IgG3 MAb 4197X linked to  
CC ricin-A and a hexa-histidine tag. The DNA construct encoding the  
CC immunotoxin was expressed from pHB19 in E. coli.  
XX (Updated on 25-MAR-2003 to correct PN field.)  
XX SQ Sequence 554 AA;  
Query Match 98.3%; Score 934.5; DB 16; Length 554;  
Best Local Similarity 93.4%; Pred. No. 6e-91; Indels 13; Gaps 1;  
Matches 185; Conservative 0; Mismatches 0;

QY 1 IFPKQYPIINFTTAGATVQSYTNFIRAVGRGLT-----NRVGLPINQRFILV 47  
 Db |||||  
 278 IFPKQYPIINFTTAGATVQSYTNFIRAVGRGLTGGADVHEIPVLNVRVGLPINQRFILV 337  
 QY 48 ELSNHAELSVTALDVTNAYVVGVRAGNSAYFFPHDPNQEDAETHLFTDVQNRYYTFAFG 107  
 Db |||||  
 338 ELSNHAELSVTALDVTNAYVVGVRAGNSAYFFPHDPNQEDAETHLFTDVQNRYYTFAFG 397  
 QY 108 GNYDRLEQAGNLRNIELGNGPLEEALISALYYSTGGTQGLPTLARSFIIQMISEAR 167  
 Db 398 GNYDRLEQAGNLRNIELGNGPLEEALISALYYSTGGTQGLPTLARSFIIQMISEAR 457  
 QY 168 FOYIEGEMTRIRYNRRS 185  
 Db 458 FOYIEGEMTRIRYNRRS 475  
 RESULT 9  
 AAP90079  
 ID AAP90079 standard; protein; 562 AA.  
 XX  
 AC AAP90079;  
 XX  
 XX 25-MAR-2003 (updated)  
 DT 01-NOV-1989 (first entry)  
 XX  
 XX Ricin D.  
 XX Ricin D; Ricinus communis; castor beans; Zanicbariensis variety;  
 KW modified; lectin binding removed; reduced cell binding  
 XX Ricinus communis (castor beans).  
 OS  
 XX WO8904839-A.  
 PN  
 XX 01-JUN-1989.  
 PD  
 XX 23-NOV-1988; 88WO-US04238.  
 PF  
 XX 24-NOV-1987; 87US-0124735.  
 PR  
 XX (GEMY ) GENETICS INST INC.  
 PA  
 XX Brown EL, Jones S;  
 PI  
 XX WPI; 1989-178366/24.  
 DR N-PSDB; AAN90068.  
 XX Modified ricin molecules and toxin conjugates  
 PT - in which the lectin binding function of the B chain  
 PT is removed or diminished to reduce cell binding.  
 XX Disclosure; fig 1; 51pp; English.  
 PS  
 XX Ricin D (see corresp. AAN90068) found on the EcoRI-HindIII fragment  
 CC of DNA from Ricinus communis, Zanicbariensis variety. Patent  
 CC discloses many modifications of ricin in which the lectin binding  
 CC function of the B chain is diminished or removed, and conjugation  
 CC to toxins to eliminate cell binding  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 CC (Updated on 25-MAR-2003 to correct PI field.)  
 XX  
 XX Sequence 562 AA;  
 Query Match 98.3%; Score 934.5; DB 10; Length 562;  
 Best Local Similarity 93.4%; Pred. No. 6.1e-91;  
 Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;  
 QY 1 IFPKQYPIINFTTAGATVQSYTNFIRAVGRGLT-----NRVGLPINQRFILV 47  
 Db 36 IFPKQYPIINFTTAGATVQSYTNFIRAVGRGLTGGADVHEIPVLNVRVGLPINQRFILV 95  
 QY 48 ELSNHAELSVTALDVTNAYVVGVRAGNSAYFFPHDPNQEDAETHLFTDVQNRYYTFAFG 107

Db 96 ELSNHAELSVTALDVTNAYVVGVRAGNSAYFFPHDPNQEDAETHLFTDVQNRYYTFAFG 155  
 QY 108 GNYDRLEQAGNLRNIELGNGPLEEALISALYYSTGGTQGLPTLARSFIIQMISEAR 167  
 Db 156 GNYDRLEQAGNLRNIELGNGPLEEALISALYYSTGGTQGLPTLARSFIIQMISEAR 215  
 QY 168 FOYIEGEMTRIRYNRRS 185  
 Db 216 FOYIEGEMTRIRYNRRS 233  
 RESULT 10  
 AAP50166  
 ID AAP50166 standard; Protein; 565 AA.  
 XX  
 AC AAP50166;  
 XX  
 XX 16-OCT-1991 (first entry)  
 DT  
 XX Sequence of prepropricin encoded by pRCL617.  
 DE  
 XX Toxin; anti-tumour therapy.  
 KW  
 XX Ricinus.  
 OS  
 XX Key  
 FH Location/Qualifiers  
 FT Peptide 1..24  
 FT Protein /label= signal  
 FT Region 292..303  
 FT /label= links the C-terminus of the A chain and  
 FT the N-terminus of the B chain  
 FT Modified-site 34..36  
 FT /label= N-linked glycosylation  
 FT Modified-site 260..262  
 FT /label= N-linked glycosylation  
 FT Modified-site 398..400  
 FT /label= N-linked glycosylation  
 FT Modified-site 438..440  
 FT /label= N-linked glycosylation  
 XX  
 XX EP145111-A.  
 PN  
 XX 19-JUN-1985.  
 PD  
 XX 13-JUL-1984; 84EP-0304801.  
 DF  
 XX 13-MAR-1984; 84GB-0006569.  
 PR 15-JUL-1983; 83GB-0019265.  
 PR 15-JUL-1983; 83CH-0019265.  
 XX  
 XX (UYWA-) UNIV WARWICK.  
 PA  
 XX Lord JM, Roberts LM, Lamb FI;  
 PI WPI; 1985-148040/25.  
 DR N-PSDB; AAN50202.  
 DR  
 XX New DNA sequences coding for ricin type plant toxin - or its  
 PT mutants, and modified vectors and host microorganisms  
 PT  
 XX Disclosure; Page 30-30c; 40pp; English.  
 PS  
 XX Prepropricin is the whole polypeptide encoded by AAN50202 and the DNA  
 CC encoding this is claimed. Prepropricin is obtained from prepropricin by  
 CC removal of the AA leader sequence. The linker AA sequence which is  
 CC present in the precursor polypeptide is enzymatically removed in the  
 CC cell to separate the A and B chains, which are joined by a  
 CC disulphide bridge during the formation of the ricin molecule itself.  
 CC This linker region as well as the presumptive amino terminal leader  
 CC or signal sequence are not present in the sequences already  
 CC published by Funatsu et al.

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XX SQ Sequence 565 AA;
    Query Match 98.3%; Score 934.5; DB 6; Length 565;
    Best Local Similarity 93.4%; Pred. No. 6.1e-91;
    Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINQRFILV 47
DB 25 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTGDVDRHDPVLPNRVGLPINQRFILV 84
QY 48 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYRTFAFG 107
DB 85 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYRTFAFG 144
QY 108 GNYDRLEQLAGNLRNIELGNGLPELEAISALYYSTGGTQPLTLARSFIICQIMISEAAR 167
DB 145 GNYDRLEQLAGNLRNIELGNGLPELEAISALYYSTGGTQPLTLARSFIICQIMISEAAR 204
QY 168 FOYIEGEMRTRIRYNRRS 185
DB 205 FOYIEGEMRTRIRYNRRS 222

RESULT 11
AAG78300
ID AAG78300 standard; Protein; 565 AA.
XX AC AAG78300;
XX DT 15-NOV-2001 (first entry)
XX DE Castor bean preprorin protein (SEQ ID 1).
XX KW Castor bean plant; preprorin; ricin; A chain; B chain;
KW human immunodeficiency virus infection; HIV; toxin; antiviral agent;
KW retroviral infection; anti-HIV; virucide activity; viral protease.
XX OS Ricinus communis.
XX FH Key Location/Qualifiers
FT Peptide 1..24
FT Protein 25..290
FT Peptide /label= Ricin A chain
FT Peptide /note= "N-glycosidase"
FT Protein 291..302
FT Protein /label= Linker_peptide
FT Protein /note= "Cleared during activation of ricin"
FT Protein 303..565
FT Protein /label= Ricin B chain
FT Protein /note= "Galactose/N-acetylgalactosamine-binding lectin"
XX WO200160393-A1.
XX 23-AUG-2001.
XX 15-FEB-2001; 2001WO-US05282.
XX 16-FEB-2000; 2000US-0182759.
XX (BECH-) BECHTEL BWXT IDAHO LLC.
XX Keener WK, Ward TE;
XX WPT; 2001-581908/65.
XX N-PSDB; AAI64137.
XX Novel composition comprising toxin e.g., ricin based antiviral compound
XX useful for treating viral infections such as human immunodeficiency
XX virus infection.
XX Disclosure; Page 47-50; 66pp; English.

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XX CC The sequence relates to preprorin protein encoded by the DNA sequence
CC given in AAI64137. The invention relates to a novel toxin (e.g., ricin)
CC based antiviral agent which is toxic to virus-infected cells, but
CC non-toxic to uninfected cells. The invention has anti-HIV and virucide
CC activities. Its mechanism of action is through inactivation of cellular
CC ribosomes and enhancement of binding of the antiviral agent to galactose
CC residues on cell surfaces, and its cellular immunodeficiency virus infection
CC and other viral infections, especially retroviral infections. The
CC antiviral agent is activated in viral particles or early-stage infected
CC cells. Killing the cells upon infection and effectively preventing the
CC integration of the viral genome into the host genome thereby preventing
CC the latency/rebound problem. The agent enters all HIV susceptible cells,
CC and not just cells known to act as host cells for the virus. The
CC antiviral agent remains inert in a cell until degraded in it, unless the
CC cell is infected with the virus, where the viral protease activates it.
XX SQ Sequence 565 AA;

    Query Match 98.3%; Score 934.5; DB 22; Length 565;
    Best Local Similarity 93.4%; Pred. No. 6.1e-91;
    Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINQRFILV 47
DB 25 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTGDVDRHDPVLPNRVGLPINQRFILV 84
QY 48 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYRTFAFG 107
DB 85 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYRTFAFG 144
QY 108 GNYDRLEQLAGNLRNIELGNGLPELEAISALYYSTGGTQPLTLARSFIICQIMISEAAR 167
DB 145 GNYDRLEQLAGNLRNIELGNGLPELEAISALYYSTGGTQPLTLARSFIICQIMISEAAR 204
QY 168 FOYIEGEMRTRIRYNRRS 185
DB 205 FOYIEGEMRTRIRYNRRS 222

RESULT 12
AAG78304
ID AAG78304 standard; Protein; 565 AA.
XX AC AAG78304;
XX DT 27-NOV-2001 (first entry)
XX DE Modified castor bean preprorin (SEQ ID 10).
XX KW Castor bean plant; preprorin; ricin; A chain; B chain;
KW human immunodeficiency virus infection; HIV; toxin; antiviral agent;
KW retroviral infection; anti-HIV; virucide; viral protease.
XX OS Chimeric - Ricinus communis
XX OS Chimeric - Human immunodeficiency virus type 2.
XX FH Key Location/Qualifiers
FT Peptide 1..24
FT Protein 25..565
FT Protein /label= Signal_peptide
FT Protein /label= Prorin
FT Protein /note= "Prorin consists of the ricin A chain, a linker
FT Protein 25..291 peptide, and the ricin B chain. Prorin is
FT Protein /label= Ricin A chain proteolytically cleaved between the A chain and
FT Protein /note= "N-glycosidase" the linker to yield mature ricin"
FT Protein 292..303
FT Protein /label= Linker_peptide
FT Cleavage-site 296..297

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FT Protein /label= HIV\_protease\_cleavage\_site  
 FT 304..565  
 FT /label= Ricin B chain  
 FT /note= "Galactose/N-acetylgalactosamine-binding lectin"  
 XX  
 PN WO200160393-A1.  
 XX  
 PD 23-AUG-2001.  
 XX  
 PF 15-FEB-2001; 2001WO-US05282.  
 XX  
 PR 16-FEB-2000; 2000US-0182759.  
 XX  
 PA (BECH-) BECHTEL BWXT IDAHO LLC.  
 XX  
 XX Keener WK, Ward TE;  
 XX  
 XX WPI; 2001-581908/65.  
 DR N-PSDB; AA164145.  
 XX  
 XX Novel composition comprising toxin e.g., ricin based antiviral compound  
 PT useful for treating viral infections such as human immunodeficiency  
 PT virus infection.  
 XX  
 XX Example 1; Page 59-63; 66pp; English.  
 XX  
 CC The sequence relates to the amino acid sequence of a modified prepropricin  
 CC protein encoded by AA164145. The invention relates to a novel toxin  
 CC (e.g. ricin) based antiviral agent which is toxic to virus-infected  
 CC cells, but non-toxic to uninfected cells. The invention has anti-HIV and  
 CC virucide activities. The agent is able to enter all HIV susceptible  
 CC cells, and not just cells known to act as host cells for the virus. The  
 CC antiviral agent remains inert in a cell unless the cell is infected  
 CC with the HIV virus, where the viral protease activates it. Ricin's  
 CC mechanism of action is through inactivation of cellular ribosomes and  
 CC enhancement of binding of the antiviral agent to galactose residues on  
 CC cell surfaces, and its cellular internalization. The invention is useful  
 CC for treating human immunodeficiency virus infection and other viral  
 CC infections, especially retroviral infections. The antiviral agent is  
 CC activated in viral particles or early-stage infected cells, killing the  
 CC cells upon infection and effectively preventing the integration of the  
 CC viral genome into the host genome thereby preventing the latency/rebound  
 CC problem.  
 XX  
 SQ Sequence 565 AA;  
 Query Match 98.3%; Score 934.5; DB 22; Length 565;  
 Best Local Similarity 93.4%; Pred. No. 6.1e-91;  
 Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;  
 QY 1 IFPKQYPIINFNTAGATVQSYTNFIRAVRGLT-----NRVGLPINQRFILV 47  
 Db 25 IFPKQYPIINFNTAGATVQSYTNFIRAVRGLTGGADVRHEIPVLPNVRGLPINQRFILV 84  
 QY 48 ELSNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDNQEDAEAIHLFTDVQNRYYTFAFG 107  
 Db 85 ELSNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDNQEDAEAIHLFTDVQNRYYTFAFG 144  
 QY 108 GNYDRLEQLAGNLRNENIELGNGLPBEAISALYYSTGGTQPLTARSFFIICQMISEAR 167  
 Db 145 GNYDRLEQLAGNLRNENIELGNGLPBEAISALYYSTGGTQPLTARSFFIICQMISEAR 204  
 QY 168 FOYIEGEMRTRIRYNRS 185  
 Db 205 FOYIEGEMRTRIRYNRS 222  
 RESULT 13  
 AAP70326  
 ID AAP70326 standard; Protein; 576 AA.  
 XX  
 AC AAP70326;  
 XX

DT 25-MAR-2003 (updated)  
 DT 21-MAY-1991 (first entry)  
 XX  
 DE Sequence of Ricinus communis (castor bean) Ricin toxin  
 DE (RT or ricin) E precursor encoded by PRT38.  
 XX  
 KW Lectin; toxin protein; cytotoxic; cytostatic; castor bean;  
 KW plant toxin.  
 XX  
 OS Ricinus communis.  
 XX  
 FH Key Location/Qualifiers  
 FH Region 1..35  
 FT /note= "leader"  
 FT 36..302  
 FT /note= "A-chain"  
 FT 315..576  
 FT /note= "B-chain"  
 XX  
 PN EP237676-A.  
 XX  
 XX 23-SEP-1987.  
 PD  
 XX 13-NOV-1986; 86EP-0308877.  
 PF  
 XX 07-MAR-1986; 86US-0837583.  
 PR  
 XX (CETU ) CETUS CORP.  
 PA (CHIR ) CHIRON CORP.  
 XX  
 PI Piatak M;  
 XX  
 DR WPI; 1987-265177/38.  
 DR N-PSDB; AA70526.  
 XX  
 XX New non-glycosylated ricin precursor and toxin etc. - are prep'd.  
 PT by recombinant DNA procedures with specific isolation steps for  
 PT purer and soluble prods.  
 XX  
 PS Disclosure; Fig 14(1-2); 112pp; English.  
 XX  
 CC The full length sequences encoding ricin A (AA70520), ricin D  
 CC (AA70525) putative ricin E (AA70526) and RCA (AA70524) in precursor  
 CC form were obtained, using the messenger RNA to obtain a cDNA library, and  
 CC then probing the library to retrieve the desired cDNA inserts. The  
 CC library was probed using the 35-mer given in AA70514. Figure 4 (see  
 CC AA70520, AA70521, AA70522), shows the nucleotide sequences of three  
 CC plasmids containing cDNA inserts obtained by probing a cDNA library  
 CC for sequences encoding ricin B using the probe in AA70517. The cDNA  
 CC inserts can be placed into expression vectors. Site-directed  
 CC mutagenesis may be used to place an ATG start codon and a HindIII  
 CC site at the beginning of the mature protein. (see AA70519). The  
 CC coding sequences of the inserts can be ligated into expression  
 CC vectors containing the Phoa promoter-operator and leader sequence  
 CC (AA70523) and suitable retroregulators.  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 576 AA;  
 Query Match 98.3%; Score 934.5; DB 8; Length 576;  
 Best Local Similarity 93.4%; Pred. No. 6.3e-91;  
 Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;  
 QY 1 IFPKQYPIINFNTAGATVQSYTNFIRAVRGLT-----NRVGLPINQRFILV 47  
 Db 36 IFPKQYPIINFNTAGATVQSYTNFIRAVRGLTGGADVRHEIPVLPNVRGLPINQRFILV 95  
 QY 48 ELSNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDNQEDAEAIHLFTDVQNRYYTFAFG 107  
 Db 96 ELSNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDNQEDAEAIHLFTDVQNRYYTFAFG 155  
 QY 108 GNYDRLEQLAGNLRNENIELGNGLPBEAISALYYSTGGTQPLTARSFFIICQMISEAR 167



Db 156 GNYDRLEQLAGNLRNIELGNGPLEEASALSYYYSTGGTQPLTLARSFIIQIMISEAAR 215

QY 168 FOYIEGEMTRIRYNRRS 185

Db 216 FOYIEGEMTRIRYNRRS 233

# RESULT 14

AAW25787  
ID AAW25787 standard; Protein; 576 AA.

XX AC AAW25787;

XX DT 25-MAR-2003 (updated)

DT 27-MAR-1998 (first entry)

XX DE Castorbean ricin.

XX KW Ricin; cytotoxin; hybrid protein; cell delivery;

KW cell binding ligand; translocation domain; diphtheria toxin B';  
KW interleukin-2; T-cell lymphoma; organ rejection; therapy.

XX OS Ricinus communis.

EH Key Location/Qualifiers

FT Peptide 1..35

FT Protein /label= sig\_peptide

FT Peptide 36..302

FT Peptide /label= A-domain

FT Peptide 303..314

FT Domain /label= Linker

FT FT 315..576

FT FT /label= B-domain

XX US5668255-A.

PN 16-SEP-1997.

PD 04-AUG-1993; 93US-0102387.

XX 27-JUN-1991; 91US-0722484.

PR 07-JUN-1984; 84US-0618199.

PR 25-APR-1985; 85US-0728808.

PR 07-JUN-1985; 85US-0742554.

PR 22-DEC-1989; 89US-0456095.

PR 14-JUN-1990; 90US-0538276.

PR 04-AUG-1993; 93US-0102387.

XX (SERA-) SERAGEN INC.

PA Murphy JR;

PI WPI; 1997-470103/43.

XX N-PSDB; AAT91638.

XX New hybrid molecules for delivery of agents to cells - comprise a

PT binding domain of a cell binding ligand and a portion of a

PT translocation domain of a protein

XX Example 4; Fig 11A-B; 30pp; English.

XX This polypeptide comprises the castorbean cytotoxin, ricin.

CC DNA (see AAT91638) encoding the enzymatic A domain and a portion

CC of the A-to-B linker peptide of ricin was used to construct a

CC ricin-diphtheria toxin B'-interleukin-2 gene that was expressed in

CC E. coli. The hybrid protein can be isolated and used to treat

CC conditions involving over-production of cells bearing IL2 receptors,

CC such as certain T-cell lymphomas and organ transplant rejection

CC crises. The hybrid inactivates ribosomes in cells bearing IL2

CC receptors, resulting in cessation of protein synthesis and death of

CC target cells. Claimed hybrid proteins comprise a translocation

CC domain and a cell binding domain from e.g. a hormone, growth factor

CC or polypeptide toxin. The hybrid molecules can be used for the

CC delivery of agents (e.g. therapeutic genes, toxins, detectable  
CC labels) into cells. The use of a translocation mechanism ensures  
CC that the hybrid will be effective in relatively low doses, since a  
CC high proportion of the substance of interest will be taken into the  
CC targeted cells. The hybrid molecules can be manufactured as a  
CC single hybrid recombinant protein, permitting reproducibility,  
CC consistency, and the precise control of composition.

CC (Updated on 25-MAR-2003 to correct PF field.)

XX SQ Sequence 576 AA;

Query Match 98.3%; Score 934.5; DB 18; Length 576;

Best Local Similarity 93.4%; Pred. No. 6.3e-91;

Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 IFFKQYPIINFETTAGATVQSYTNFIRAVRGRIT-----NRVGLPINQRFILV 47

Db 36 IFFKQYPIINFETTAGATVQSYTNFIRAVRGRITGADVRHEIPVLPNRVGLPINQRFILV 95

QY 48 ELSNHAELSVTLALDVTNAYVGVYAGNSAYFFHEDNQEDAEATHLFTDVQNRVTFAPG 107

Db 96 ELSNHAELSVTLALDVTNAYVGVYAGNSAYFFHEDNQEDAEATHLFTDVQNRVTFAPG 155

QY 108 GNYDRLEQLAGNLRNIELGNGPLEEASALSYYYSTGGTQPLTLARSFIIQIMISEAAR 167

Db 156 GNYDRLEQLAGNLRNIELGNGPLEEASALSYYYSTGGTQPLTLARSFIIQIMISEAAR 215

QY 168 FOYIEGEMTRIRYNRRS 185

Db 216 FOYIEGEMTRIRYNRRS 233

## RESULT 15

AAW55892

ID AAW55892 standard; Protein; 576 AA.

XX AC AAW55892;

XX DT 15-FEB-2000 (first entry)

XX DE Castor bean ricin toxin.

XX KW Recombinant; hybrid; binding domain; ligand; animal cell; diphtheria;

XX translocation domain; botulinum; neurotoxin; ricin; cholera; tetanus;

XX shiga-like toxin; pertussis; translocation; cytoplasmic membrane; HIV;

XX cytosol; therapy; genetic deficiency disease; enzyme; co-factor; poison;

XX adipocyte; cancer; virus; infection; antibody.

XX OS Ricinus communis.

XX US5965406-A.

XX PD 12-OCT-1999.

XX PF 07-JUN-1995; 95US-0488246.

XX PR 04-AUG-1993; 93US-0102387.

PR 07-JUN-1984; 84US-0618199.

PR 27-JUN-1991; 91US-0722484.

PR 25-APR-1985; 85US-0728808.

PR 07-JUN-1985; 85US-0742554.

PR 22-DEC-1989; 89US-0456095.

PR 14-JUN-1990; 90US-0538276.

XX (SERA-) SERAGEN INC.

PA Murphy JR;

PI WPI; 1999-632431/54.

XX N-PSDB; AAZ30663.

XX Recombinant DNA molecule encoding a three part hybrid protein used in

PT the treatment of Aids and genetic deficiency diseases -

XX  
PS  
XX

Example 4; Fig 11; 31pp; English.

XX The invention relates to a recombinant DNA molecule encoding a hybrid protein comprising three parts: (a) the first part comprises a portion of the binding domain of a cell-binding polypeptide ligand allowing the hybrid protein to bind to an animal cell; (b) the second part comprises a portion of a translocation domain of a naturally occurring protein selected from diphtheria toxin, botulinum neurotoxin, ricin, cholera toxin, LT toxin, C3 toxin, shiga-like toxin, pertussis toxin and tetanus toxin, which translocate the third part of the across the cytoplasmic membrane into the cytosol of the cell; and (c) the third part comprises a polypeptide entity to be introduced into the cell, which is non-native to the naturally occurring protein of (b). This sequence represents the Castor bean ricin toxin sequence for use in generating the hybrid of the invention. The hybrid molecule enables the direction of appropriate therapy to affected cells, allowing them to function properly and alleviate or cure the disease. The hybrid is especially used in treating genetic deficiency diseases, by delivering to affected cells an enzyme supplying the missing function, to supplementing cellular levels of a particular enzyme or a scarce precursor or cofactor, to directing toxins or other poisons to destroy particular cells (such as adipocytes, cancer cell, or virus infected-cells), to counteracting viral infections such as HIV, by introducing appropriate antibodies to viral proteins. It is also involved in the process of getting non-therapeutic substances such as detectable labels into cells.

XX SQ Sequence 576 AA;

Query Match 98.3%; Score 934.5; DB 20; Length 576;  
 Best Local Similarity 93.4%; Pred. No. 6.3e-91;  
 Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY	1	IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINQRFILV	47
Db	36	IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTGTADVRHEIPVLPNRVGLPINQRFILV	95
QY	48	ELSNHAELSVTLALDVNTNAYVGVYRAGNSAYFFHPDQDEAEATHTLFTDVQNYTFAPG	107
Db	96	ELSNHAELSVTLALDVNTNAYVGVYRAGNSAYFFHPDQDEAEATHTLFTDVQNYTFAPG	155
QY	108	GNVDRLEQLAGNLRNIELNGNPLEEASIALYVYSTGCTQPLTLARSFIICQMISEAAR	167
Db	156	GNVDRLEQLAGNLRNIELNGNPLEEASIALYVYSTGCTQPLTLARSFIICQMISEAAR	215
QY	168	FOYIEGEMTRIRYNRRS	185
Db	216	FOYIEGEMTRIRYNRRS	233

Search completed: February 10, 2004, 16:22:28  
 Job time : 31.5419 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:18:30 ; Search time 10.6968 Seconds  
(without alignments)  
731.761 Million cell updates/sec

Title: US-10-083-336A-9

Perfect score: 951

Sequence: 1 IFPKQYPIINTTAGATVQS.....ARFQVIEGEMETRYNRS 185

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A COMB.pap:\*  
2: /cgn2\_6/ptodata/1/iaa/5B COMB.pap:\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pap:\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pap:\*  
5: /cgn2\_6/ptodata/1/iaa/PTCUS COMB.pap:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	934.5	98.3	267	1	US-07-901-707-1
2	934.5	98.3	267	1	US-07-988-430-1
3	934.5	98.3	267	1	US-08-425-336-1
4	934.5	98.3	267	1	US-08-488-113B-1
5	934.5	98.3	267	1	US-08-477-484B-1
6	934.5	98.3	267	2	US-08-646-360-1
7	934.5	98.3	267	3	US-08-839-765-1
8	934.5	98.3	267	3	US-09-136-389-1
9	934.5	98.3	267	4	US-09-610-838-1
10	934.5	98.3	267	5	PCT-US92-09487-1
11	934.5	98.3	268	2	US-08-356-786-8
12	934.5	98.3	290	1	US-08-378-761A-27
13	934.5	98.3	290	1	US-08-485-286-27
14	934.5	98.3	290	6	5248606-4
15	934.5	98.3	534	2	US-08-356-786-10
16	924.5	97.2	267	1	US-08-218-303-16
17	924.5	97.2	267	2	US-08-338-793D-61
18	924.5	97.2	267	4	US-09-538-873-1
19	845	88.9	540	1	US-08-378-761A-77
20	845	88.9	540	1	US-08-485-286-77
21	337.5	35.5	247	1	US-08-488-113B-6
22	337.5	35.5	247	1	US-08-477-484B-6
23	337.5	35.5	247	3	US-08-646-360-6
24	337.5	35.5	247	3	US-08-839-765-6
25	337.5	35.5	247	3	US-09-136-389-6
26	337.5	35.5	247	4	US-09-610-838-6
27	337.5	35.5	267	1	US-08-378-761A-74

28 337.5 35.5 267 1 US-08-485-286-74  
29 337.5 35.5 289 1 US-07-923-692C-4  
30 337.5 35.5 289 1 US-08-184-237-4  
31 337.5 35.5 289 2 US-08-482-920-4  
32 337.5 35.5 289 3 US-08-484-341-4  
33 337.5 35.5 289 3 US-08-483-502-4  
34 337.5 35.5 289 4 US-09-726-651A-4  
35 312 32.8 255 1 US-07-901-707-6  
36 312 32.8 255 1 US-07-988-430-6  
37 312 32.8 255 1 US-08-425-336-6  
38 312 32.8 255 5 PCT-US92-09487-6  
39 312 32.8 282 1 US-08-324-301-15  
40 300.5 31.6 248 3 US-08-902-486-7  
41 300.5 31.6 290 1 US-08-245-754A-2  
42 300.5 31.6 290 2 US-08-597-731-2  
43 300.5 31.6 496 3 US-08-902-486-15  
44 291 30.6 250 1 US-08-378-761A-71  
45 291 30.6 250 1 US-08-485-286-71

## ALIGNMENTS

RESULT 1  
US-07-901-707-1  
; Sequence 1, Application US/07901707  
; Patent No. 5376546  
; GENERAL INFORMATION:  
; APPLICANT: Bernhardt, Susan L.  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Steve F.  
; APPLICANT: Lane, Julie A.  
; TITLE OF INVENTION: Materials Comprising and Methods of  
; TITLE OF INVENTION: Composition and Use for Ribosome-Inactivating Proteins  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Bicknell,  
; STREET: Two first National Plaza, 20 South Clark  
; STREET: Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/901.707  
; FILING DATE: 19920619  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5376546and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27129/30910  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 346-5750  
; TELEFAX: (312) 984-5750  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 267 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-901-707-1

Query Match 98.3%; Score 934.5; DB 1; Length 267;

Best Local Similarity 93.4%; Pred. No. 1.1e-101;  
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINQRFILV 47  
DB 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTGADVRHEIPVLPNRVGLPINQRFILV 60

QY 48 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEAIHTLFTDVQNRYYTFAFG 107  
DB 61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEAIHTLFTDVQNRYYTFAFG 120

QY 108 GNYDRLEQLAGNRENIELGNGLPBEAISALYYSTGGTQPLTLARSFIIQIMISEAAR 167  
DB 121 GNYDRLEQLAGNRENIELGNGLPBEAISALYYSTGGTQPLTLARSFIIQIMISEAAR 180

QY 168 FOYIEGEMTRIRYNRRS 185  
DB 181 FOYIEGEMTRIRYNRRS 198

RESULT 2  
US-07-988-430-1  
; Sequence 1, Application US/07988430  
; Patent No. 5416202  
; GENERAL INFORMATION:  
; APPLICANT: Bernhard, Susan L.  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Lane, Julie A.  
; APPLICANT: Lei, Shau-Ping  
; TITLE OF INVENTION: Materials Comprising and Methods of  
; Preparation and Use for Ribosome-Inactivating Proteins  
; NUMBER OF SEQUENCES: 101  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Bicknell  
; STREET: Two First National Plaza, 20 South Clark  
; STREET: Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/988,430  
; FILING DATE: 19921209  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5416202and, Greta E.  
; REGISTRATION NUMBER: 35302  
; REFERENCE/DOCKET NUMBER: 31133  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 346-5750  
; TELEFAX: (312) 984-9740  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 267 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-988-430-1

Query Match 98.3%; Score 934.5; DB 1; Length 267;  
Best Local Similarity 93.4%; Pred. No. 1.1e-101;  
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINQRFILV 47  
DB 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTGADVRHEIPVLPNRVGLPINQRFILV 60

QY 48 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEAIHTLFTDVQNRYYTFAFG 107  
DB 61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEAIHTLFTDVQNRYYTFAFG 120

QY 108 GNYDRLEQLAGNRENIELGNGLPBEAISALYYSTGGTQPLTLARSFIIQIMISEAAR 167  
DB 121 GNYDRLEQLAGNRENIELGNGLPBEAISALYYSTGGTQPLTLARSFIIQIMISEAAR 180

QY 168 FOYIEGEMTRIRYNRRS 185  
DB 181 FOYIEGEMTRIRYNRRS 198

RESULT 3  
US-08-425-336-1  
; Sequence 1, Application US/08425336  
; Patent No. 5621083  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; TITLE OF INVENTION: Proteins  
; NUMBER OF SEQUENCES: 140  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/425,336  
; FILING DATE: 18-APR-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/064,691  
; FILING DATE: 12-MAY-1993  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meyers, Thomas C.  
; REGISTRATION NUMBER: P-36,989  
; REFERENCE/DOCKET NUMBER: 31394  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 267 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-425-336-1

Query Match 98.3%; Score 934.5; DB 1; Length 267;

Best Local Similarity 93.4%; Pred. No. 1.1e-101;  
 Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;  
 Qy 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINORFILV 47  
 Db 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTGGADVREHPVLPNKRVLGINORFILV 60  
 Qy 48 ELSNHAELSVTLADVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYTFAFG 107  
 Db 61 ELSNHAELSVTLADVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYTFAFG 120  
 Qy 108 GNYDRLEQLAGNLRNIELGNGLPELEAISALYYSTGGTQTLPTLARSFIICQMISEAAR 167  
 Db 121 GNYDRLEQLAGNLRNIELGNGLPELEAISALYYSTGGTQTLPTLARSFIICQMISEAAR 180  
 Qy 168 FOYIEGEMRTRIRYNRRS 185  
 Db 181 FOYIEGEMRTRIRYNRRS 198

## RESULT 4

US-08-488-113B-1  
 ; Sequence 1, Application US/08488113B  
 ; Patent No. 574580  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Better, Marc D.  
 ; APPLICANT: Carroll, Stephen F.  
 ; APPLICANT: Studnika, Gary M.  
 ; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
 ; NUMBER OF SEQUENCES: 169  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
 ; STREET: 500 West Madison Street, 34th floor  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: USA  
 ; ZIP: 60661  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/488,113B  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 530  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/425,336  
 ; FILING DATE: 18-APR-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/064,691  
 ; FILING DATE: 12-MAY-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/988,430  
 ; FILING DATE: 09-DEC-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/901,707  
 ; FILING DATE: 19-JUN-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/787,567  
 ; FILING DATE: 04-NOV-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: McNicholas, Janet M.  
 ; REGISTRATION NUMBER: 32,918  
 ; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
 ; TELEPHONE: 312/707-8889  
 ; TELEFAX: 312/707-9155  
 ; TELEX: 650 388-1248  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 267 amino acids

; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-488-113B-1  
 Query Match 98.3%; Score 934.5; DB 1; Length 267;  
 Best Local Similarity 93.4%; Pred. No. 1.1e-101;  
 Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;  
 Qy 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINORFILV 47  
 Db 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTGGADVREHPVLPNKRVLGINORFILV 60  
 Qy 48 ELSNHAELSVTLADVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYTFAFG 107  
 Db 61 ELSNHAELSVTLADVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYTFAFG 120  
 Qy 108 GNYDRLEQLAGNLRNIELGNGLPELEAISALYYSTGGTQTLPTLARSFIICQMISEAAR 167  
 Db 121 GNYDRLEQLAGNLRNIELGNGLPELEAISALYYSTGGTQTLPTLARSFIICQMISEAAR 180  
 Qy 168 FOYIEGEMRTRIRYNRRS 185  
 Db 181 FOYIEGEMRTRIRYNRRS 198

RESULT 5  
 US-08-477-484B-1  
 ; Sequence 1, Application US/08477484B  
 ; Patent No. 5756699  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Better, Marc D.  
 ; APPLICANT: Carroll, Stephen F.  
 ; APPLICANT: Studnika, Gary M.  
 ; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
 ; NUMBER OF SEQUENCES: 169  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
 ; STREET: 500 West Madison Street, 34th floor  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: USA  
 ; ZIP: 60661  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/477,484B  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 530  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/425,336  
 ; FILING DATE: 18-APR-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/064,691  
 ; FILING DATE: 12-MAY-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/988,430  
 ; FILING DATE: 09-DEC-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/901,707  
 ; FILING DATE: 19-JUN-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/787,567  
 ; FILING DATE: 04-NOV-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: McNicholas, Janet M.  
 ; REGISTRATION NUMBER: 32,918  
 ; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
 ; TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
REGISTRATION NUMBER: 32,918  
INFORMATION FOR SEQ ID NO: 1:  
REFERENCE/DOCKET NUMBER: 200-70.P4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 267 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-477-494B-1

Query Match 98.3%; Score 934.5; DB 1; Length 267;  
Best Local Similarity 93.4%; Pred. No. 1.1e-101;  
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;  
QY 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINQRFILV 47  
DB 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTGGADVRHEIPVLPNVRGLPINQRFILV 60  
QY 48 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEAIHTLFTDVQNYRTFAFG 107  
DB 61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEAIHTLFTDVQNYRTFAFG 120  
QY 108 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIQIMISEAAR 167  
DB 121 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIQIMISEAAR 180  
QY 168 FOYIEGEMTRIRYNRRS 185  
DB 181 FOYIEGEMTRIRYNRRS 198

## RESULT 6

US-08-646-360-1  
Sequence 1, Application US/08646360  
Patent No. 5837491

GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,360  
FILING DATE: 13-MAY-1996  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PC/US94/05348  
FILING DATE: 12-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70.P4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 267 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-646-360-1

Query Match 98.3%; Score 934.5; DB 2; Length 267;  
Best Local Similarity 93.4%; Pred. No. 1.1e-101;  
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;  
QY 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINQRFILV 47  
DB 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTGGADVRHEIPVLPNVRGLPINQRFILV 60  
QY 48 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEAIHTLFTDVQNYRTFAFG 107  
DB 61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEAIHTLFTDVQNYRTFAFG 120  
QY 108 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIQIMISEAAR 167  
DB 121 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIQIMISEAAR 180  
QY 168 FOYIEGEMTRIRYNRRS 185  
DB 181 FOYIEGEMTRIRYNRRS 198

## RESULT 7

US-08-839-765-1  
Sequence 1, Application US/08839765  
Patent No. 6146631

GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/839,765  
FILING DATE: 15-APR-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/425,336  
FILING DATE: 18-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430

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/ FILING DATE: 09-DEC-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-8889
/ TELEFAX: 312/707-9155
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 267 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-839-765-1

Query Match      98.3%; Score 934.5; DB 3; Length 267;
Best Local Similarity 93.4%; Pred. No. 1.1e-101;
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 IPFKQYPIINFTTAGATVQSYTNFIRAVGRLLT-----NRVGLPINQRFILV 47
Db 1 IPFKQYPIINFTTAGATVQSYTNFIRAVGRLLTGADVRHEIPVLPNRVGLPINQRFILV 60
QY 48 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYTFAFG 107
Db 61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYTFAFG 120
QY 108 GNYDRLEQLAGNLRNENIELGNGLPLEEASALYYSTGGTOLPTLARSFICIQMISEAAR 167
Db 121 GNYDRLEQLAGNLRNENIELGNGLPLEEASALYYSTGGTOLPTLARSFICIQMISEAAR 180
QY 168 FOYIEGEMTRIRYNRRS 185
Db 181 FOYIEGEMTRIRYNRRS 198

RESULT 8
US-09-136-389-1
; Sequence 1, Application US/09136389
; Patent No. 6146850
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/646,360

/ FILING DATE: 13-MAY-1996
/ APPLICATION NUMBER: PCT/US94/05348
/ FILING DATE: 12-MAY-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/064,691
/ FILING DATE: 12-MAY-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-DEC-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ APPLICATION DATA:
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 200-70.P4
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/707-8889
/ TELEFAX: 312/707-9155
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 267 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-136-389-1

Query Match      98.3%; Score 934.5; DB 3; Length 267;
Best Local Similarity 93.4%; Pred. No. 1.1e-101;
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 IPFKQYPIINFTTAGATVQSYTNFIRAVGRLLT-----NRVGLPINQRFILV 47
Db 1 IPFKQYPIINFTTAGATVQSYTNFIRAVGRLLTGADVRHEIPVLPNRVGLPINQRFILV 60
QY 48 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYTFAFG 107
Db 61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYTFAFG 120
QY 108 GNYDRLEQLAGNLRNENIELGNGLPLEEASALYYSTGGTOLPTLARSFICIQMISEAAR 167
Db 121 GNYDRLEQLAGNLRNENIELGNGLPLEEASALYYSTGGTOLPTLARSFICIQMISEAAR 180
QY 168 FOYIEGEMTRIRYNRRS 185
Db 181 FOYIEGEMTRIRYNRRS 198

RESULT 9
US-09-610-838-1
; Sequence 1, Application US/09610838
; Patent No. 6376217
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/646,360
```

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/610,838
; FILING DATE: 06-JUL-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
; FILING DATE: 18-AUG-1998
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70-P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-610-838-1

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Query Match      98.3%; Score 934.5; DB 4; Length 267;
Best Local Similarity 93.4%; Pred. No. 1.1e-101;
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINQRFILV 47
Db 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTGGADVRHEIPVLPNVRVGLPINQRFILV 60
QY 48 ELSNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQEDAEALTHLFTDVQNYTFAFG 107
Db 61 ELSNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQEDAEALTHLFTDVQNYTFAFG 120
QY 108 GNYDRLEQLAGNLRNLELNGPLLEEAISALYYSTGGTQPLTLARSFIIQIMISEAAR 167
Db 121 GNYDRLEQLAGNLRNLELNGPLLEEAISALYYSTGGTQPLTLARSFIIQIMISEAAR 180
QY 168 FOYIEGEMTRIRYNRRS 185
Db 181 FOYIEGEMTRIRYNRRS 198

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RESULT 10
PCT-US92-09487-1
; Sequence 1, Application PC/TUS9209487
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping
; TITLE OF INVENTION: Materials Comprising and Methods of
; Preparation and Use for Ribosome-Inactivating Proteins

```

```

; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09487
; FILING DATE: 19921104
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35302
; REFERENCE/DOCKET NUMBER: 31133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US92-09487-1

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Query Match      98.3%; Score 934.5; DB 5; Length 267;
Best Local Similarity 93.4%; Pred. No. 1.1e-101;
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINQRFILV 47
Db 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTGGADVRHEIPVLPNVRVGLPINQRFILV 60
QY 48 ELSNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQEDAEALTHLFTDVQNYTFAFG 107
Db 61 ELSNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQEDAEALTHLFTDVQNYTFAFG 120
QY 108 GNYDRLEQLAGNLRNLELNGPLLEEAISALYYSTGGTQPLTLARSFIIQIMISEAAR 167
Db 121 GNYDRLEQLAGNLRNLELNGPLLEEAISALYYSTGGTQPLTLARSFIIQIMISEAAR 180
QY 168 FOYIEGEMTRIRYNRRS 185
Db 181 FOYIEGEMTRIRYNRRS 198

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RESULT 11
US-08-356-786-8
; Sequence 8, Application US/08356786
; Patent No. 5877305
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
; Marker

```



NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault  
STREET: Exchange Place, 53 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/356,786  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/831,967  
FILING DATE: 06-FEB-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Pitcher, Edmund R.  
REGISTRATION NUMBER: 27,829  
REFERENCE/DOCKET NUMBER: CRP-053  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 268 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-356-786-8

Query Match 98.3%; Score 934.5; DB 2; Length 268;  
Best Local Similarity 93.4%; Pred. No. 1.1e-101;  
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;  
QY 1 IFFKQYPIINFTTAGATVQSYTNFIRAVRGLT-----NRVGLPINQRFILV 47  
DB 2 IFFKQYPIINFTTAGATVQSYTNFIRAVRGLTGGADVRHEIPVLPNRVGLPINQRFILV 61  
QY 48 ELSNHAELSVTLADVTNAYVVGVRAGNSAYFFHPDQDAEAITHLFTDVQNRYYTFAFG 107  
DB 62 ELSNHAELSVTLADVTNAYVVGVRAGNSAYFFHPDQDAEAITHLFTDVQNRYYTFAFG 121  
QY 108 GNYDRLEQLAGNLRNIELGNGPLEEAISALYYSTGGTQGLPTLARSFFIICQMISEAAR 167  
DB 122 GNYDRLEQLAGNLRNIELGNGPLEEAISALYYSTGGTQGLPTLARSFFIICQMISEAAR 181  
QY 168 FOYIEGEMTRIRYNRRS 185  
DB 182 FOYIEGEMTRIRYNRRS 199  
RESULT 12  
US-08-378-761A-27  
Sequence 27, Application US/08378761A  
Patent No. 5635384  
GENERAL INFORMATION:  
APPLICANT: WALSH, TERENCE A  
APPLICANT: HEY, TIMOTHY D  
APPLICANT: MORGAN, ALICE ER  
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE  
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF  
TITLE OF INVENTION: USING  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ANDREA T. BORUCKI  
STREET: 9330 ZIONSVILLE ROAD  
CITY: INDIANAPOLIS  
STATE: IN

COUNTRY: US  
ZIP: 46268  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/378,761A  
FILING DATE: 26-JAN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BORUCKI, ANDREA T  
REGISTRATION NUMBER: 33651  
REFERENCE/DOCKET NUMBER: 38272B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 337-4846  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 290 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-378-761A-27  
Query Match 98.3%; Score 934.5; DB 1; Length 290;  
Best Local Similarity 93.4%; Pred. No. 1.3e-101;  
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;  
QY 1 IFFKQYPIINFTTAGATVQSYTNFIRAVRGLT-----NRVGLPINQRFILV 47  
DB 25 IFFKQYPIINFTTAGATVQSYTNFIRAVRGLTGGADVRHEIPVLPNRVGLPINQRFILV 84  
QY 48 ELSNHAELSVTLADVTNAYVVGVRAGNSAYFFHPDQDAEAITHLFTDVQNRYYTFAFG 107  
DB 85 ELSNHAELSVTLADVTNAYVVGVRAGNSAYFFHPDQDAEAITHLFTDVQNRYYTFAFG 144  
QY 108 GNYDRLEQLAGNLRNIELGNGPLEEAISALYYSTGGTQGLPTLARSFFIICQMISEAAR 167  
DB 145 GNYDRLEQLAGNLRNIELGNGPLEEAISALYYSTGGTQGLPTLARSFFIICQMISEAAR 204  
QY 168 FOYIEGEMTRIRYNRRS 185  
DB 205 FOYIEGEMTRIRYNRRS 222  
RESULT 13  
US-08-485-286-27  
Sequence 27, Application US/08485286  
Patent No. 5646026  
Patent No. 5646026 5646119  
GENERAL INFORMATION:  
APPLICANT: WALSH, TERENCE A  
APPLICANT: HEY, TIMOTHY D  
APPLICANT: MORGAN, ALICE ER  
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE  
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF  
TITLE OF INVENTION: USING  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ANDREA T. BORUCKI  
STREET: 9330 ZIONSVILLE ROAD  
CITY: INDIANAPOLIS  
STATE: IN  
COUNTRY: US  
ZIP: 46268  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,286  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION NUMBER: US 08/378761  
FILING DATE: 26-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: BORUCKI, ANDREA T  
REGISTRATION NUMBER: 33651  
REFERENCE/DOCKET NUMBER: 38272B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (317) 337-4846  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 290 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-485-286-27

Query Match 98.3%; Score 934.5; DB 1; Length 290;  
Best Local Similarity 93.4%; Pred. No. 1.3e-101;  
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;  
QY 1 IPPKQYPIINFTTAGATVQSYTNFIRAVGRGLT-----NRVGLPINQRFILV 47  
DB 25 IPPKQYPIINFTTAGATVQSYTNFIRAVGRGLTTGADVVRHEIPVLPNVRVGLPINQRFILV 84  
QY 48 ELSNHAELSVTALDVTNAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDVQNRVTFAG 107  
DB 85 ELSNHAELSVTALDVTNAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDVQNRVTFAG 144  
QY 108 GNYDRLEQLAGNLRNIELGNGLPDEEASALYYSTGGTQPLTARSFFIICQMISEAAR 167  
DB 145 GNYDRLEQLAGNLRNIELGNGLPDEEASALYYSTGGTQPLTARSFFIICQMISEAAR 204  
QY 168 FOYIEGEMTRIRYNRRS 185  
DB 205 FOYIEGEMTRIRYNRRS 222

RESULT 14  
5248606-4  
Patent No. 5248606  
APPLICANT: WALSH, TERENCE A.; HEY, TIMOTHY D.; MORGAN,  
ALICE E.R.  
TITLE OF INVENTION: DNA ENCODING INACTIVE PRECURSOR AND  
ACTIVE FORMS OF MAIZE RIBOSOME INACTIVATION  
NUMBER OF SEQUENCES: 49  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/535,636  
FILING DATE: 11-JUN-1990  
SEQ ID NO: 4  
LENGTH: 290  
5248606-4

Query Match 98.3%; Score 934.5; DB 6; Length 290;  
Best Local Similarity 93.4%; Pred. No. 1.3e-101;  
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;  
QY 1 IPPKQYPIINFTTAGATVQSYTNFIRAVGRGLT-----NRVGLPINQRFILV 47  
DB 25 IPPKQYPIINFTTAGATVQSYTNFIRAVGRGLTTGADVVRHEIPVLPNVRVGLPINQRFILV 84  
QY 48 ELSNHAELSVTALDVTNAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDVQNRVTFAG 107  
DB 85 ELSNHAELSVTALDVTNAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDVQNRVTFAG 144  
QY 108 GNYDRLEQLAGNLRNIELGNGLPDEEASALYYSTGGTQPLTARSFFIICQMISEAAR 167  
DB 145 GNYDRLEQLAGNLRNIELGNGLPDEEASALYYSTGGTQPLTARSFFIICQMISEAAR 204

QY 168 FOYIEGEMTRIRYNRRS 185  
DB 205 FOYIEGEMTRIRYNRRS 222  
RESULT 15  
US-08-356-786-10  
Sequence 10, Application US/08356786  
Patent No. 5877305  
GENERAL INFORMATION:  
APPLICANT: Huston, James S.  
APPLICANT: Oppermann, Hermann  
APPLICANT: Houston, L. L.  
APPLICANT: Ring, David B.  
TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer  
TITLE OF INVENTION: Marker  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault  
STREET: Exchange Place, 53 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/356,786  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/831,967  
FILING DATE: 06-FEB-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Pitcher, Edmund R.  
REGISTRATION NUMBER: 27,829  
REFERENCE/DOCKET NUMBER: CRP-053  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 534 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-356-786-10

Query Match 98.3%; Score 934.5; DB 2; Length 534;  
Best Local Similarity 93.4%; Pred. No. 3.1e-101;  
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 IPPKQYPIINFTTAGATVQSYTNFIRAVGRGLT-----NRVGLPINQRFILV 47  
DB 4 IPPKQYPIINFTTAGATVQSYTNFIRAVGRGLTTGADVVRHEIPVLPNVRVGLPINQRFILV 63  
QY 48 ELSNHAELSVTALDVTNAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDVQNRVTFAG 107  
DB 64 ELSNHAELSVTALDVTNAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDVQNRVTFAG 123  
QY 108 GNYDRLEQLAGNLRNIELGNGLPDEEASALYYSTGGTQPLTARSFFIICQMISEAAR 167  
DB 124 GNYDRLEQLAGNLRNIELGNGLPDEEASALYYSTGGTQPLTARSFFIICQMISEAAR 183  
QY 168 FOYIEGEMTRIRYNRRS 185  
DB 184 FOYIEGEMTRIRYNRRS 201

Search completed: February 10, 2004, 16:29:34

us-10-083-336a-9.rai

Sun Feb 15 07:30:06 2004

Job time : 11.6968 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:26:46 ; Search time 23.8621 Seconds  
(without alignments)  
1623.314 Million cell updates/sec

Title: US-10-083-336A-9

Perfect score: 951

Sequence: 1 IFPKQVPIINFTTAGATVQS.....ARFQYIEGEMRTRIRYNRRS 185

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubaa/US06\_PUBCOMB.pep.\*
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- 6: /cgn2\_6/ptodata/1/pubaa/PCTUS\_PUBCOMB.pep.\*
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- 10: /cgn2\_6/ptodata/1/pubaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				Description	
Result No.	Score	Match	Length DB ID		
1	951	100.0	185	12	US-10-083-336A-9 Sequence 9, Appli
2	939.5	98.8	188	12	US-10-083-336A-4 Sequence 4, Appli
3	939.5	98.8	189	12	US-10-083-336A-6 Sequence 6, Appli
4	939.5	98.8	190	12	US-10-083-336A-11 Sequence 11, Appli
5	934.5	98.3	198	12	US-10-083-336A-3 Sequence 3, Appli
6	934.5	98.3	199	12	US-10-083-336A-5 Sequence 5, Appli
7	934.5	98.3	200	12	US-10-083-336A-10 Sequence 10, Appli
8	934.5	98.3	267	12	US-10-127-890-1 Sequence 1, Appli
9	934.5	98.3	576	12	US-10-083-336A-1 Sequence 1, Appli
10	929.5	97.7	188	12	US-10-083-336A-8 Sequence 8, Appli
11	924.5	97.2	198	12	US-10-083-336A-7 Sequence 7, Appli
12	924.5	97.2	267	12	US-10-282-935-1 Sequence 1, Appli
13	924.5	97.2	267	12	US-10-440-796-1 Sequence 1, Appli
14	662.5	69.7	179	12	US-10-083-336A-2 Sequence 2, Appli
15	337.5	35.5	247	10	US-09-792-793A-39 Sequence 39, Appli

16	337.5	35.5	247	12	US-10-127-890-6 Sequence 6, Appli
17	337.5	35.5	247	12	US-10-375-209A-39 Sequence 39, Appli
18	337.5	35.5	289	12	US-10-280-679B-4 Sequence 4, Appli
19	330.5	31.6	247	10	US-09-792-793A-34 Sequence 34, Appli
20	300.5	31.6	247	12	US-10-375-209A-34 Sequence 34, Appli
21	285	30.0	251	12	US-10-282-935-3 Sequence 3, Appli
22	285	30.0	251	12	US-10-440-796-3 Sequence 3, Appli
23	270.5	28.4	263	12	US-10-127-890-7 Sequence 7, Appli
24	268.5	28.2	263	12	US-10-127-890-4 Sequence 4, Appli
25	262.5	27.6	252	9	US-09-347-064-2 Sequence 2, Appli
26	262.5	27.6	252	9	US-09-347-064-8 Sequence 8, Appli
27	259	27.2	248	12	US-10-127-890-5 Sequence 5, Appli
28	241	25.3	251	12	US-10-127-890-107 Sequence 107, App
29	240	25.2	251	12	US-10-127-890-106 Sequence 106, App
30	240	25.2	251	12	US-10-127-890-110 Sequence 110, App
31	240	25.2	251	12	US-10-127-890-111 Sequence 111, App
32	239	25.1	251	9	US-09-765-527-247 Sequence 247, App
33	239	25.1	251	12	US-10-127-890-2 Sequence 2, Appli
34	239	25.1	251	12	US-10-127-890-99 Sequence 99, Appli
35	239	25.1	251	12	US-10-127-890-100 Sequence 100, App
36	239	25.1	251	12	US-10-127-890-101 Sequence 101, App
37	239	25.1	251	12	US-10-127-890-102 Sequence 102, App
38	239	25.1	251	12	US-10-127-890-103 Sequence 103, App
39	239	25.1	251	12	US-10-127-890-104 Sequence 104, App
40	239	25.1	251	12	US-10-127-890-105 Sequence 105, App
41	239	25.1	316	12	US-10-074-596-1 Sequence 1, Appli
42	239	25.1	507	12	US-10-074-596-11 Sequence 11, Appli
43	238	25.0	251	12	US-10-127-890-109 Sequence 109, App
44	238	25.0	293	9	US-09-765-527-259 Sequence 259, App
45	238	25.0	309	9	US-09-765-527-253 Sequence 253, App

ALIGNMENTS

RESULT 1

US-10-083-336A-9  
; Sequence 9, Application US/10083336A  
; Publication No. US20030181665A1  
; GENERAL INFORMATION:  
; APPLICANT: Olsson, Mark A  
; APPLICANT: Millard, Charles B  
; APPLICANT: Byrne, Michael P  
; APPLICANT: Wannemacher, Robert W  
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof  
; FILE REFERENCE: P67452US0 (RIID 01-58)  
; CURRENT APPLICATION NUMBER: US/10/083,336A  
; CURRENT FILING DATE: 2002-05-21  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 185  
; TYPE: PRT  
; ORGANISM: Ricinus communis  
US-10-083-336A-9

Query Match				100.0%; Score 951; DB 12; Length 185;			
Best Local Similarity				100.0%; Pred. No. 1.5e-101;			
Matches 185; Conservative				0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	IFPKQVPIINFTTAGATVQS	YTFIRAVGRGLNRVGLPINQRFILVELSNHAE	SVTLA	60		
Db	1	IFPKQVPIINFTTAGATVQS	YTFIRAVGRGLNRVGLPINQRFILVELSNHAE	SVTLA	60		
Qy	61	LDVTNAYVVGVRAGNSAYFFH	PDNQDEAEATHLFTDVQNR	YTFAFGNGYDRLEQLAGN	120		
Db	61	LDVTNAYVVGVRAGNSAYFFH	PDNQDEAEATHLFTDVQNR	YTFAFGNGYDRLEQLAGN	120		
Qy	121	RENIEIENGPLEBAISALYY	YSTGGTQLPTLARSFFI	CIOMISEAARFQYIEGEM	TRIR 180		
Db	121	RENIEIENGPLEBAISALYY	YSTGGTQLPTLARSFFI	CIOMISEAARFQYIEGEM	TRIR 180		
Qy	181	YNRRS	185				

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Db      181 YNRRS 185
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RESULT 2
US-10-083-336A-4
; Sequence 4, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-4

Query Match      98.8%; Score 939.5; DB 12; Length 188;
Best Local Similarity 98.4%; Pred. No. 3.2e-100;
Matches 185; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY      1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT---NRVGLPINQRFILVELSNHAELSV 57
Db      1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT---NRVGLPINQRFILVELSNHAELSV 60
QY      58 TLALDVNTNAYVVGVRAGNSAYFFHPDNQEDAEAI THLFTDVQNRVYTFAGGNYDRLEQLA 117
Db      61 TLALDVNTNAYVVGVRAGNSAYFFHPDNQEDAEAI THLFTDVQNRVYTFAGGNYDRLEQLA 120
QY      118 GNLENIELGNGLPBEAISALYYSTGGTOLPTLARSFIIICMISEARFOYIEGEMRT 177
Db      121 GNLENIELGNGLPBEAISALYYSTGGTOLPTLARSFIIICMISEARFOYIEGEMRT 180
QY      178 RIRYNRRS 185
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Db      181 RIRYNRRS 188
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RESULT 3
US-10-083-336A-6
; Sequence 6, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-6

Query Match      98.8%; Score 939.5; DB 12; Length 189;
Best Local Similarity 98.4%; Pred. No. 3.2e-100;
Matches 185; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY      1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT---NRVGLPINQRFILVELSNHAELSV 57
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Db      1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT---NRVGLPINQRFILVELSNHAELSV 57
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QY      58 TLALDVNTNAYVVGVRAGNSAYFFHPDNQEDAEAI THLFTDVQNRVYTFAGGNYDRLEQLA 117
Db      61 TLALDVNTNAYVVGVRAGNSAYFFHPDNQEDAEAI THLFTDVQNRVYTFAGGNYDRLEQLA 120
QY      118 GNLENIELGNGLPBEAISALYYSTGGTOLPTLARSFIIICMISEARFOYIEGEMRT 177
Db      121 GNLENIELGNGLPBEAISALYYSTGGTOLPTLARSFIIICMISEARFOYIEGEMRT 180
QY      178 RIRYNRRS 185
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Db      181 RIRYNRRS 188
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RESULT 4
US-10-083-336A-11
; Sequence 11, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-11

Query Match      98.8%; Score 939.5; DB 12; Length 190;
Best Local Similarity 98.4%; Pred. No. 3.3e-100;
Matches 185; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY      1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT---NRVGLPINQRFILVELSNHAELSV 57
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QY      58 TLALDVNTNAYVVGVRAGNSAYFFHPDNQEDAEAI THLFTDVQNRVYTFAGGNYDRLEQLA 117
Db      62 TLALDVNTNAYVVGVRAGNSAYFFHPDNQEDAEAI THLFTDVQNRVYTFAGGNYDRLEQLA 121
QY      118 GNLENIELGNGLPBEAISALYYSTGGTOLPTLARSFIIICMISEARFOYIEGEMRT 177
Db      122 GNLENIELGNGLPBEAISALYYSTGGTOLPTLARSFIIICMISEARFOYIEGEMRT 181
QY      178 RIRYNRRS 185
|||||
Db      182 RIRYNRRS 189
|||||

RESULT 5
US-10-083-336A-3
; Sequence 3, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3

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; LENGTH: 198
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-3

Query Match      98.3%; Score 934.5; DB 12; Length 198;
Best Local Similarity 93.4%; Pred. No. 1.3e-99;
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 IFPKQYPIINFNTAGATVQSYTNFIRAVGRLLT-----NRVGLPINQRFILV 47
Db 1 IFPKQYPIINFNTAGATVQSYTNFIRAVGRLLTGDVREHPIVLPNVRVGLPINQRFILV 60

QY 48 ELSNHAELSVTLLADVTNAYVVGVRAGNSAYFFHPDNOQEDAEATHLFTDVQVRYTFAFG 107
Db 61 ELSNHAELSVTLLADVTNAYVVGVRAGNSAYFFHPDNOQEDAEATHLFTDVQVRYTFAFG 120

QY 108 GNYDRLEQLAGNLRENIELGNGPLEEASALYYSTGGTQPLTARSFIIQIMISEAAR 167
Db 121 GNYDRLEQLAGNLRENIELGNGPLEEASALYYSTGGTQPLTARSFIIQIMISEAAR 180

QY 168 FOYIEGEMTRIRYNRRS 185
Db 181 FOYIEGEMTRIRYNRRS 198

RESULT 6
US-10-083-336A-5
; Sequence 5, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-5

Query Match      98.3%; Score 934.5; DB 12; Length 199;
Best Local Similarity 93.4%; Pred. No. 1.3e-99;
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 IFPKQYPIINFNTAGATVQSYTNFIRAVGRLLT-----NRVGLPINQRFILV 47
Db 2 IFPKQYPIINFNTAGATVQSYTNFIRAVGRLLTGDVREHPIVLPNVRVGLPINQRFILV 61

QY 48 ELSNHAELSVTLLADVTNAYVVGVRAGNSAYFFHPDNOQEDAEATHLFTDVQVRYTFAFG 107
Db 62 ELSNHAELSVTLLADVTNAYVVGVRAGNSAYFFHPDNOQEDAEATHLFTDVQVRYTFAFG 121

QY 108 GNYDRLEQLAGNLRENIELGNGPLEEASALYYSTGGTQPLTARSFIIQIMISEAAR 167
Db 122 GNYDRLEQLAGNLRENIELGNGPLEEASALYYSTGGTQPLTARSFIIQIMISEAAR 181

QY 168 FOYIEGEMTRIRYNRRS 185
Db 182 FOYIEGEMTRIRYNRRS 199

RESULT 7
US-10-083-336A-10
; Sequence 10, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-10

Query Match      98.3%; Score 934.5; DB 12; Length 200;
Best Local Similarity 93.4%; Pred. No. 1.3e-99;
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 IFPKQYPIINFNTAGATVQSYTNFIRAVGRLLT-----NRVGLPINQRFILV 47
Db 2 IFPKQYPIINFNTAGATVQSYTNFIRAVGRLLTGDVREHPIVLPNVRVGLPINQRFILV 61

QY 48 ELSNHAELSVTLLADVTNAYVVGVRAGNSAYFFHPDNOQEDAEATHLFTDVQVRYTFAFG 107
Db 62 ELSNHAELSVTLLADVTNAYVVGVRAGNSAYFFHPDNOQEDAEATHLFTDVQVRYTFAFG 121

QY 108 GNYDRLEQLAGNLRENIELGNGPLEEASALYYSTGGTQPLTARSFIIQIMISEAAR 167
Db 122 GNYDRLEQLAGNLRENIELGNGPLEEASALYYSTGGTQPLTARSFIIQIMISEAAR 181

QY 168 FOYIEGEMTRIRYNRRS 185
Db 182 FOYIEGEMTRIRYNRRS 199

RESULT 8
US-10-127-890-1
; Sequence 1, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/127,890
; FILING DATE: 23-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992

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; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-127-890-1

Query Match      98.3%; Score 934.5; DB 12; Length 267;
Best Local Similarity 93.4%; Pred. No. 2e-99;
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINQRFILV 47
DB 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTGGADVRRHEIPVLPNRVGLPINQRFILV 60
QY 48 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAG 107
DB 61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAG 120
QY 108 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQLTPLTARSFFIICQMISEAAR 167
DB 121 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQLTPLTARSFFIICQMISEAAR 180
QY 168 FOYIEGEMTRIRYNRRS 185
DB 181 FOYIEGEMTRIRYNRRS 198

RESULT 9
US-10-083-336A-1
; Sequence 1, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrnes, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-1

Query Match      98.3%; Score 934.5; DB 12; Length 576;
Best Local Similarity 93.4%; Pred. No. 6e-99;
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINQRFILV 47
DB 36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTGGADVRRHEIPVLPNRVGLPINQRFILV 95
QY 48 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAG 107
DB 181 FOYIEGEMTRIRYNRRS 198

US-10-083-336A-7
; Sequence 7, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrnes, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 7
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-7

Query Match      97.7%; Score 929.5; DB 12; Length 188;
Best Local Similarity 98.4%; Pred. No. 4.6e-99;
Matches 183; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT---NRVGLPINQRFILVLSNHAELSVTL 59
DB 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVLSNHAELSVTL 62
QY 60 ALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAGGNYDRLEQLAGN 119
DB 63 ALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAGGNYDRLEQLAGN 122
QY 120 LRENIELGNGLPLEEASALYYSTGGTQLTPLTARSFFIICQMISEAARFOYIEGEMTRIRI 179
DB 123 LRENIELGNGLPLEEASALYYSTGGTQLTPLTARSFFIICQMISEAARFOYIEGEMTRIRI 182
QY 180 RYNRRS 185
DB 183 RYNRRS 188

RESULT 11
US-10-083-336A-8
; Sequence 8, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrnes, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 8
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-8

Query Match      97.7%; Score 929.5; DB 12; Length 188;
Best Local Similarity 98.4%; Pred. No. 4.6e-99;
Matches 183; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT---NRVGLPINQRFILVLSNHAELSVTL 59
DB 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVLSNHAELSVTL 62
QY 60 ALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAGGNYDRLEQLAGN 119
DB 63 ALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAGGNYDRLEQLAGN 122
QY 120 LRENIELGNGLPLEEASALYYSTGGTQLTPLTARSFFIICQMISEAARFOYIEGEMTRIRI 179
DB 123 LRENIELGNGLPLEEASALYYSTGGTQLTPLTARSFFIICQMISEAARFOYIEGEMTRIRI 182
QY 180 RYNRRS 185
DB 183 RYNRRS 188

RESULT 10
US-10-083-336A-8
; Sequence 8, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrnes, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 8
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-8

Query Match      97.7%; Score 929.5; DB 12; Length 188;
Best Local Similarity 98.4%; Pred. No. 4.6e-99;
Matches 183; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT---NRVGLPINQRFILVLSNHAELSVTL 59
DB 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVLSNHAELSVTL 62
QY 60 ALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAGGNYDRLEQLAGN 119
DB 63 ALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAGGNYDRLEQLAGN 122
QY 120 LRENIELGNGLPLEEASALYYSTGGTQLTPLTARSFFIICQMISEAARFOYIEGEMTRIRI 179
DB 123 LRENIELGNGLPLEEASALYYSTGGTQLTPLTARSFFIICQMISEAARFOYIEGEMTRIRI 182
QY 180 RYNRRS 185
DB 183 RYNRRS 188

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Query Match 97.2%; Score 924.5; DB 12; Length 198;  
Best Local Similarity 93.4%; Pred. No. 1.9e-98;  
Matches 183; Conservative 0; Mismatches 0; Indels 13; Gaps 1;  
  
QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINORFILVEL 49  
DB 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINORFILVEL 62  
  
QY 50 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 109  
DB 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 122  
  
QY 110 YDRLEQAGNLRNIELNGPLPEEAISALYYSTGGTQPTLARSFIIICIMISEAARFQ 169  
DB 123 YDRLEQAGNLRNIELNGPLPEEAISALYYSTGGTQPTLARSFIIICIMISEAARFQ 182  
  
QY 170 YIEGEMTRIRYNRRS 185  
DB 183 YIEGEMTRIRYNRRS 198

## RESULT 12

US-10-282-935-1  
; Sequence 1, Application US/10282935  
; Publication No. US20030143193A1  
; GENERAL INFORMATION:  
; APPLICANT: VITETTA, ELLEN S.  
; APPLICANT: GHETTIE, VICTOR F.  
; APPLICANT: SMALLSHAW, JOAN  
; APPLICANT: BALUNA, ROXANA G.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF  
; TITLE OF INVENTION: PROTEINACEOUS COMPOUNDS  
; FILE REFERENCE: UTSD:884US  
; CURRENT APPLICATION NUMBER: US/10/282,935  
; CURRENT FILING DATE: 2002-10-29  
; PRIOR APPLICATION NUMBER: 09/538,873  
; PRIOR FILING DATE: 2000-03-30  
; PRIOR APPLICATION NUMBER: 60/126,826  
; PRIOR FILING DATE: 1999-03-30  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 267  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-10-282-935-1

Query Match 97.2%; Score 924.5; DB 12; Length 267;  
Best Local Similarity 93.4%; Pred. No. 2.9e-98;  
Matches 183; Conservative 0; Mismatches 0; Indels 13; Gaps 1;  
  
QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINORFILVEL 49  
DB 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINORFILVEL 62  
  
QY 50 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 109  
DB 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 122  
  
QY 110 YDRLEQAGNLRNIELNGPLPEEAISALYYSTGGTQPTLARSFIIICIMISEAARFQ 169  
DB 123 YDRLEQAGNLRNIELNGPLPEEAISALYYSTGGTQPTLARSFIIICIMISEAARFQ 182  
  
QY 170 YIEGEMTRIRYNRRS 185  
DB 183 YIEGEMTRIRYNRRS 198

## RESULT 13

Query Match 69.7%; Score 662.5; DB 12; Length 179;  
Best Local Similarity 91.0%; Pred. No. 2.9e-68;  
Matches 131; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

US-10-440-796-1  
; Sequence 1, Application US/10440796  
; Publication No. US20040009148A1  
; GENERAL INFORMATION:  
; APPLICANT: VITETTA, ELLEN S.  
; APPLICANT: GHETTIE, VICTOR F.  
; APPLICANT: SMALLSHAW, JOAN  
; APPLICANT: BALUNA, ROXANA G.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK  
; TITLE OF INVENTION: SYNDROME (VLS)  
; FILE REFERENCE: UTSD:603  
; CURRENT APPLICATION NUMBER: US/10/440,796  
; CURRENT FILING DATE: 2003-05-19  
; PRIOR APPLICATION NUMBER: US/09/538,873  
; PRIOR FILING DATE: 2000-03-30  
; PRIOR APPLICATION NUMBER: 60/126,826  
; PRIOR FILING DATE: 1999-03-30  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 267  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-10-440-796-1

Query Match 97.2%; Score 924.5; DB 12; Length 267;  
Best Local Similarity 93.4%; Pred. No. 2.9e-98;  
Matches 183; Conservative 0; Mismatches 0; Indels 13; Gaps 1;  
  
QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINORFILVEL 49  
DB 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINORFILVEL 62  
  
QY 50 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 109  
DB 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 122  
  
QY 110 YDRLEQAGNLRNIELNGPLPEEAISALYYSTGGTQPTLARSFIIICIMISEAARFQ 169  
DB 123 YDRLEQAGNLRNIELNGPLPEEAISALYYSTGGTQPTLARSFIIICIMISEAARFQ 182  
  
QY 170 YIEGEMTRIRYNRRS 185  
DB 183 YIEGEMTRIRYNRRS 198

## RESULT 14

US-10-083-336A-2  
; Sequence 2, Application US/10083336A  
; Publication No. US20030181665A1  
; GENERAL INFORMATION:  
; APPLICANT: Olson, Mark A  
; APPLICANT: Millard, Charles B  
; APPLICANT: Byrnes, Michael P  
; APPLICANT: Wannemacher, Robert W  
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof  
; FILE REFERENCE: P67452US0 (RIID 01-58)  
; CURRENT APPLICATION NUMBER: US/10/083,336A  
; CURRENT FILING DATE: 2002-05-21  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 179  
; TYPE: PRT  
; ORGANISM: Ricinus communis  
US-10-083-336A-2



1	IFPKQYPIINFTTAGATVQSTNFI	RAVRGSLT-----NRVGLPINQREFILV	47
	DB		
36	IFPKQYPIINFTTAGATVQSTNFI	RAVRGSLTTGADVREIIPVLPNVRVGLPINQREFILV	95
	DB		
48	ELSNHAEI.SVTLALDVTNAYVVG	VRAGNSAYFFHPDNCQEDAEAI	107
	DB		
96	ELSNHAEI.SVTLALDVTNAYVVG	VRAGNSAYFFHPDNCQEDAEAI	155
	DB		
108	GNYDRLEQLAGNLRENIEI	LGNGPL	131
	DB		
156	GNYDRLEQLAGNLRENIEI	LGNGPL	179
	DB		

RESULT 15  
US-09-792-793A-39  
; Sequence 39, Application US/09792793A  
; Patent No. US20020168370A1  
; GENERAL INFORMATION:  
; APPLICANT: McDonald, John R.  
; APPLICANT: Coggins, Philip  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND  
; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS  
; FILE REFERENCE: 25020-601D  
; CURRENT APPLICATION NUMBER: US/09/792,793A  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 93  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 39  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: Trichosantheus kirilowii  
US-09-792-793A-39

Query Match	35.5%;	Score 337.5;	DB 10;	Length 247;
Best local similarity	39.0%;	Pred. No. 1.6e-30;		
Matches	71;	Conservative 42;	Mismatches 50;	Indels 19; Gaps 4;
QY	9	INFTTAGATVQSNTNFIRAVRGLTN-----RVGLPINORFPLVLSNHAELSVT	58	
DB	2	VSPFLSGATSSGVFTSNRKALPNERKLYDTPLESPLGSGQRVALIHLTVVADETIS	61	
QY	59	LALDVTNAYVVGVRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAPGGNTRLEQLA	117	
DB	62	VALIDVTNVITMGVRAGTSYFF--NEASATEAAKYVKDMRKVTLPYSGNYERLTAA	118	
QY	118	GNARENTELCNGPLEEAI SALYYSTCGTGTOPLTLARSFICIMISAARFQYEGBMRT	177	
DB	119	GKURENPILGPLDCAISAITLFYYNAN-----SAASALMWLIQSTSEARKYKTEQQIGK	173	
QY	178	RI	179	
DB	174	KV	175	

Search completed: February 10, 2004, 16:53:54  
Job time : 23.8621 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2004, 16:17:35 ; Search time 10.0111 Seconds  
(without alignments)  
1777.145 Million cell updates/sec

Title: US-10-083-336A-9

Perfect score: 951

Sequence: 1 IFPKQPIINFTTAGTVQS.....ARFQIEGEMRTIRNRRS 185

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76:\*

1: Pir1: \*  
2: Pir2: \*  
3: Pir3: \*  
4: Pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	934.5	98.3	576	1 RLCSO	ricin D precursor
2	845	88.9	564	1 RLCSAG	agglutinin precurs
3	337.5	35.5	289	1 RUTZT	rRNA N-glycosidase
4	327.5	34.4	247	2 JU0393	karasurin - Mongol
5	327.5	34.4	247	2 JU0332	karasurin-B - Tric
6	327.5	34.4	289	2 JU0306	karasurin C - Tric
7	317	33.3	528	2 S22431	abrin-d precursor
8	317	33.3	562	2 S16022	abrin-c precursor
9	316.5	33.3	527	2 S23430	abrin-b precursor
10	310	32.6	251	2 C39761	abrin (clone 7.2)
11	297	31.2	278	2 S23519	beta-luffin - smoo
12	291	30.6	528	1 T2LSA	abrin-a precursor
13	290	30.5	250	2 JN0108	luffin-b - smooth
14	276	29.0	277	2 S22494	rRNA N-glycosidase
15	272.5	28.7	254	2 P00118	mistletoe lectin I
16	270.5	28.4	286	1 RLPUGG	rRNA N-glycosidase
17	268.5	28.2	286	2 S25560	rRNA N-glycosidase
18	268.5	28.2	570	2 S26227	agglutinin I precu
19	266.5	28.0	245	2 JU4840	rRNA N-glycosidase
20	261.5	27.5	286	2 JU4235	rRNA N-glycosidase
21	239	25.1	316	2 JU0753	rRNA N-glycosidase
22	184	19.3	294	2 S28421	rRNA N-glycosidase
23	177.5	18.7	278	2 A39817	rRNA N-glycosidase
24	168.5	17.7	313	2 S17557	rRNA N-glycosidase
25	167	17.6	261	2 JE0401	antiviral protein
26	150	15.8	289	2 T12573	rRNA N-glycosidase
27	138.5	14.6	272	2 JU4811	betavulgin - beet
28	131.5	13.8	253	2 S28542	rRNA N-glycosidase
29	127.5	13.4	253	2 S28539	rRNA N-glycosidase

#### ALIGNMENTS

##### RESULT 1

###### RLCSO

ricin D precursor - castor bean

N;Contains: rRNA N-glycosidase (EC 3.2.2.22)

C;Species: Ricinus communis (castor bean)

C;Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text change 16-Jul-1999

C;Accession: A24041; S20513; A24614; A03372; A24010; A03374; S10903

R;Halling, K.C.; Halling, A.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F.

Nucleic Acids Res. 13, 8019-8033, 1985

A;Title: Genomic cloning and characterization of a ricin gene from Ricinus communis.

A;Reference number: A24041; MUID:86067214; PMID:2999712

A;Accession: A24041

A;Molecule type: DNA

A;Residues: 1-576 <HAL>

A;Cross-references: GB:X03179; NID:g21082; PIDN:CAA26939.1; PID:g21083

R;Tregear, J.W.; Roberts, L.M.

Plant Mol. Biol. 18, 515-525, 1992

A;Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene

A;Reference number: S20513; MUID:92163016; PMID:1371405

A;Accession: S20513

A;Molecule type: DNA

A;Residues: 1-576 <TRE>

A;Cross-references: EMBL:X52908; NID:g21084; PIDN:CAA37095.1; PID:g21085

R;Lamb, F.I.; Roberts, L.M.; Lord, J.M.

Eur. J. Biochem. 148, 265-270, 1985

A;Title: Nucleotide sequence of cloned cDNA coding for prepropricin.

A;Reference number: A24614; MUID:85179479; PMID:3838723

A;Accession: A24614

A;Molecule type: mRNA

A;Residues: 12-75, 'D', 77-550, 'R', 552-576 <LAM>

A;Cross-references: GB:X02388; NID:g21077; PIDN:CAA26230.1; PID:g21078

R;Yoshitake, S.; Funatsu, G.; Funatsu, M.

Agric. Biol. Chem. 42, 1267-1274, 1978

A;Title: Isolation and sequences of peptic peptides, and the complete sequence of ile cha

A;Reference number: A03372

A;Accession: A03372

A;Molecule type: protein

A;Residues: 36-97, 'Q', 99-109, 'S', 111-269, 'D', 272-283, 'L', 285-288, 290-302 <YOS>

A;Note: this paper cites the others in the series providing experimental details for the

R;Araki, T.; Funatsu, G.

FEBS Lett. 191, 121-124, 1985

A;Title: Revised amino acid sequence of the B-chain of ricin D due to loss of tryptophan

A;Reference number: A24010

A;Accession: A24010

A;Molecule type: protein

A;Residues: 315-383, 'PS', 386-576 <ARA>

R;Funatsu, G.; Kimura, M.; Funatsu, M.

Agric. Biol. Chem. 43, 2221-2224, 1979

A;Title: Primary structure of Ala chain of ricin D.

A;Reference number: A03374

A;Accession: A03374

A;Molecule type: protein

A;Residues: 315-335, 'N', 337-342, 'NH', 345-362, 364-383, 'PS', 386-399, 'T', 401, 'D', 403, 'E', 405-551, 'V', 553-527, 'E', 529-564, 'W', 566, 'H', 567-570, 'LT', 573-574, 'F' <FUN>  
A;Note: This paper, one of a series, summarizes the experimental details for the determination of the complete amino acid sequence of the B-chain of the Ricinus communis agglutinin.  
R;Ready, M.P.; Kim, Y.; Robertus, J.D.  
Proteins 10, 270-278, 1991  
A;Title: Site-directed mutagenesis of ricin A-chain and implications for the mechanism of ricin toxicity.  
A;Reference number: A48237; PMID:91352006; PMID:1881883  
A;Contents: annotation; active site  
R;Rutenber, E.; Robertus, J.D.  
Proteins 10, 260-269, 1991  
A;Title: Structure of ricin B-chain at 2.5 angstrom resolution.  
A;Reference number: A48238; PMID:91352005; PMID:1881882  
A;Contents: annotation; X-ray crystallography, 2.5 angstroms  
R;Katzin, B.J.; Collins, E.J.; Robertus, J.D.  
Proteins 10, 251-259, 1991  
A;Title: Structure of ricin A-chain at 2.5 angstroms.  
A;Reference number: A48239; PMID:91352004; PMID:1881881  
A;Contents: annotation; X-ray crystallography, 2.5 angstroms  
C;Comment: The functional molecule is a disulfide-linked dimer of A and B chains, which is inactive. The A chain inhibits protein synthesis; it inactivates the 60S ribosomal subunit of the cell of the A chain; B chains are also responsible for cell agglutination (lectin).  
C;Comment: This protein is cytotoxic and very poisonous to animals.  
C;Superfamily: ricin; rRNA N-glycosidase homology  
C;Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed  
F;1-35/Domain: signal sequence #status predicted <SIG>  
F;36-302/Product: ricin D chain A #status experimental <ACH>  
F;46-293/Domain: rRNA N-glycosidase homology <RNG>  
F;315-576/Product: ricin D chain B #status experimental <BCH>  
F;331-373, 374-414, 417-455, 462-497, 501-540, 543-576/Region: 40-residue repeats  
F;45, 409, 449/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F;115, 158, 243, 244/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted  
F;212/Active site: Glu #status experimental  
F;215/Active site: Arg #status predicted  
F;294-318, 334-353, 377-394, 465-478, 504-521/Disulfide bonds: #status experimental  
F;336, 349, 360/Binding site: N-acetylgalactosamine (Asp, Gln, Asn) #status experimental  
F;548, 569/Binding site: N-acetylgalactosamine (Asp, Asn) #status experimental

Query Match 98.3%; Score 934.5; DB 1; Length 576;  
Best Local Similarity 93.4%; Pred. No. 2.3e-78;  
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;  
  
QY 1 IPPKQYPIINFNTAGATVQSYTNFIRAVRGLT-----NRVGLPINQRFILV 47  
Db 36 IPPKQYPIINFNTAGATVQSYTNFIRAVRGLTGDVVRHEIPVLPNRVGLPINQRFILV 95  
QY 48 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEAIHLFTDQVQRYTFAFG 107  
Db 96 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEAIHLFTDQVQRYTFAFG 155  
QY 108 GNYDRLEQLAGNRENIELGNGPLEEASALYYSTGGTQPLTARSFFIICQMISEAR 167  
Db 156 GNYDRLEQLAGNRENIELGNGPLEEASALYYSTGGTQPLTARSFFIICQMISEAR 215  
QY 168 FOYIEGEMRTRIRYNRRS 185  
Db 216 FOYIEGEMRTRIRYNRRS 233  
  
RESULT 2  
RLCSAG  
agglutinin precursor - castor bean  
N;Contains: rRNA N-glycosidase (EC 3.2.2.22)  
C;Species: Ricinus communis (castor bean)  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 16-Jul-1999  
C;Accession: A24261; A24210  
R;Roberts, L.M.; Lamb, I.F.; Pappin, D.J.C.; Lord, J.M.  
J. Biol. Chem. 260, 15682-15686, 1985  
A;Title: The primary sequence of Ricinus communis agglutinin. Comparison with ricin.  
A;Reference number: A24261; MUID:86059449; PMID:2999130  
A;Accession: A24261  
A;Molecule type: mRNA  
A;Residues: 1-564 <ROB>  
A;Cross-references: GB:M12089; NID:g169700; PIDN:AAA33869.1; PID:g169701

R;Araki, T.; Yoshioka, Y.; Funatsu, G.  
Biochim. Biophys. Acta 872, 277-285, 1986  
A;Title: The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin.  
A;Reference number: A24210  
A;Accession: A24210  
A;Molecule type: protein  
A;Residues: 303-325, 'F', 327-330, 'T', 332-361, 'D', 363-373, 'G', 375-403, 'T', 405-551, 'V', 553-527, 'E', 529-564, 'W', 566, 'H', 567-570, 'LT', 573-574, 'F' <FUN>  
C;Comment: This protein has strong agglutinating activity and weak cytotoxicity compared to ricin.  
C;Superfamily: ricin; rRNA N-glycosidase homology  
C;Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed  
F;1-24/Domain: signal sequence #status predicted <SIG>  
F;25-290/Product: agglutinin chain A #status predicted <ACH>  
F;35-281/Domain: rRNA N-glycosidase homology <RNG>  
F;303-564/Product: agglutinin chain B #status experimental <BCH>  
F;319-361, 362-402, 405-443, 450-485, 489-528, 531-564/Region: 40-residue repeats  
F;34, 259/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;104, 147, 231, 232/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted  
F;200, 203/Active site: Glu, Arg #status predicted  
F;282-306, 322-341, 365-382, 453-466, 492-509/Disulfide bonds: #status predicted  
F;324, 337, 348/Binding site: N-acetylgalactosamine (Asp, Gln, Asn) #status predicted  
F;397, 437/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F;536, 557/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted

Query Match 88.9%; Score 845; DB 1; Length 564;  
Best Local Similarity 85.4%; Pred. No. 4e-70;  
Matches 169; Conservative 7; Mismatches 8; Indels 14; Gaps 2;  
  
QY 1 IPPKQYPIINFNTAGATVQSYTNFIRAVRGLT-----NRVGLPINQRFILV 47  
Db 25 IPPKQYPIINFNTAGATVQSYTNFIRAVRGLTGDVVRHEIPVLPNRVGLPINQRFILV 84  
QY 48 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEAIHLFTDQVQRYTFAFG 107  
Db 85 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEAIHLFTDQVQRYTFAFG 144  
QY 108 GNYDRLEQLAGNRENIELGNGPLEEASALYYSTGGTQPLTARSFFIICQMISEAR 167  
Db 145 GNYDRLEQLAGNRENIELGNGPLEEASALYYSTGGTQPLTARSFFIICQMISEAR 203  
QY 168 FOYIEGEMRTRIRYNRRS 185  
Db 204 FOYIEGEMRTRIRYNRRS 221  
  
RESULT 3  
RLCSAG  
rRNA N-glycosidase (EC 3.2.2.22) alpha-trichosanthin precursor [validated] - Mongolian snake  
N;Alternate names: alpha-TCS; type I ribosome-inactivating protein  
C;Species: Trichosanthin kirkowii (Mongolian snake-gourd)  
C;Date: 30-Sep-1988 #sequence\_revision 26-Jan-1996 #text\_change 23-Mar-2001  
C;Accession: JT0566; A36274; JCI093; A36273; JT0003  
R;Shaw, P.C.; Yung, M.H.; Zhu, R.H.; Ho, W.K.K.; Ng, T.B.; Yeung, H.W.  
Gene 97, 267-272, 1991  
A;Title: Cloning of trichosanthin cDNA and its expression in Escherichia coli.  
A;Reference number: JT0566; MUID:91153657; PMID:1999291  
A;Accession: JT0566  
A;Molecule type: mRNA  
A;Residues: 1-289 <SHA>  
A;Cross-references: GB:M34858; NID:g170536; PIDN:AAA34207.1; PID:g170537  
R;Chow, T.P.; Feldman, R.A.; Lovett, M.; Piatak, M.  
J. Biol. Chem. 265, 8670-8674, 1990  
A;Title: Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a type I ribosome-inactivating protein.  
A;Reference number: A36274; MUID:90256790; PMID:2341400  
A;Accession: A36274  
A;Molecule type: DNA  
A;Residues: 1-233, 'T', 235-246, 'M', 248-289 <CHO>  
A;Cross-references: GB:J05434; NID:g170534; PIDN:AAA34206.1; PID:g170535  
R;Zheng, H.G.; Wang, B.; Shao, P.Z.; Yang, X.R.  
Acta Genet. Sin. 21, 42-51, 1994  
A;Title: Cloning and DNA sequencing of the gene encoding Trichosanthin.  
A;Reference number: JCI093; MUID:94271613; PMID:8003348  
A;Accession: JCI093

QY 178 RI 179  
| :  
Db 197 RV 198

RESULT 4  
JU0393  
karasurin - Mongolian snake-gourd  
C:Species: Trichosanthes kirilowii (Mongolian snake-gourd)

Query Match	34.4%	Score	327.5;	DB 2;	Length	247;			
Best Local Similarity	39.0%	Pred. No.	8.6e-23;						
Matches	71;	Conservative	42;	Mismatches	50;	Indels	19;	Gaps	4;
Qy	9	INFITAGATGVSYNFIRAVGRGLTN-----RVGLPINQRFILVELSNHAEISVT	58						
Db	2	VSFRLSGATSSYGVFISNLRKAUPLYERKLYDIPILRSTLPGSRVALLHLINAYDETIS	61						
Qy	59	LALDVNTAAVYVGYRAGNSAYFFHPDNOEDA-EAITHLFTDVQNRVYFAFGNGYDRLEQLA	117						
Db	62	VAIDVTNVVNGYRAGDTSYFF---NEASATEAAKYVFKDARKKVTLPYSGNYERLQIAA	118						
Qy	118	GNLRNIELGNGLPEEAISALYVYGTGTQLPTLARSFLICIQMISEAARFQYIEGEMRT	177						
Db	119	GKIRENIEPLGLPADSAITTLTFYNNAN-----SAASALMVLQSTSEARYKITEQOIGK	173						

Qy 178 RI 179  
|:  
Db 174 RV 175

RESULT 6

7C5606

karasurin C - Trichosanthes kirilowii var. japonica

N:Contains: karasurin A

C:Species: Trichosanthes kirilowii var. japonica

C:Date: 23-Sep-1997 #sequence\_revision 23-Sep-1997 #text\_change 19-Jul-2002

C:Accession: J05606; J05033

R:R.Mizukami, H.; Iida, K.; Kondo, T.; Ogiwara, Y.

R:Biol. Pharm. Bull. 20, 711-713, 1997

A:Title: Cloning and bacterial expression of a gene encoding ribosome-inactivating protein

A:Reference number: J05606; MUID:97356562; PMID:9212998

A:Accession: J05606

A:Molecule type: DNA

A:Residues: 1-289 <MIZ>

A:Cross-references: DBJ:AB000666; NID:92329830; PIDN:BAA21786.1; PID:92329831

R:R.Kondo, T.; Mizukami, H.; Takeda, T.; Ogiwara, Y.

R:Biol. Pharm. Bull. 19, 1485-1489, 1996

A:Title: Amino acid sequences and ribosome-inactivating activities of karasurin-B and karasurin-A

A:Reference number: J05032; MUID:97108848; PMID:8951169

A:Accession: J05033

A:Status: preliminary

A:Molecule type: protein

A:Residues: 22-270 <KON>

C:Comment: This protein is a ribosome-inactivating protein and exhibit cytotoxic, abortifacient and antiproliferative activities. This protein belongs to type I ribosomal-inactivating proteins which catalyze the N-glycosidase homology

C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology

F:22-270/Product: karasurin C #status predicted <MAC>

F:24-270/Product: karasurin A #status predicted <MAC>

F:27-266/Domain: rRNA N-glycosidase homology <RNG>

Query Match 34.4%; Score 327.5; DB 2; Length 289;

Best Local Similarity 39.0%; Pred. No. 1.1e-22;

Matches 71; Conservative 42; Mismatches 50; Indels 19; Gaps 4;

QY 9 INFTTAGATVQSYTNPIRAVRGLTN-----RVGLPINQRFILVELSNHLSVT 58

DB 25 VSFRLSGSSSSGVVFISMLRKALPYERKLYDPIILRSTLPQSQRYALHLTNYADETIS 84

QY 59 LALDVTNAVVGVRAGNSAYVEHPDQEDA-EAITHLFTDVQNRVYFAFGNVDRLEQLA 117

DB 85 VALDVTNVYMGVRAGDTSYFF---NEAGATEAKVTFKDAKKVTLPSGNGVERLQIAA 141

QY 118 GNLRNIELNGNPLEPAISALYYVYSGTGQTLPTARSFTICIMISEAARFOVIEGEMRT 177

DB 142 GXIRENIPGLPALDSAITLFFYNNAN----SAAGALMWLIQTSEARRYKFEQQIGK 196

QY 178 RI 179

DB 197 RV 198

RESULT 7

S32431

abrin-d precursor - Indian licorice (fragment)

N:Contains: rRNA N-glycosidase (EC 3.2.2.22)

C:Species: Abrus precatorius (Indian licorice)

C:Date: 30-Sep-1993 #sequence\_revision 01-Aug-1997 #text\_change 01-Aug-1997

C:Accession: S32431; S34408

R:Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.

R:J. Mol. Biol. 229, 263-267, 1993

A:Title: Primary structure of three distinct isoabirins determined by cDNA sequencing. CC

A:Reference number: S32429; MUID:93132798; PMID:8421313

A:Accession: S32431

A:Molecule type: mRNA

A:Residues: 1-528 <HUN>

A:Cross-references: GB:M98346

R:Hung, C.; Lee, M.; Lee, T.; Lin, J.

submitted to the EMBL Data Library, March 1993

A:Reference number: S34408

A:Accession: S34408

A:Molecule type: mRNA

A:Residues: 1-169 <C>, 171-320 <L>, 322-528 <HUT>





Best Local Similarity 33.2%; Pred. No. 2.5e-19;  
Matches 61; Conservative 48; Mismatches 57; Indels 18; Gaps 4;

QY 9 INFTAGATVQSYTNFIRAVRGLNTRVGLPIN-----VGLPI-----NORFILVELSNHAEISVT 58  
Db 3 VFSLSGSSSTYSKFIQDLRKALPSN-GTVYNTILLSSASGASRYTILMTLSNYDGKAI 80

QY 59 LALDVTNAYVVGYPAGNSAYFFHPDNOEDAEATHLFTDQVNRYPFAGGNYDRLEQLAG 118  
Db 63 MAIDVTNVYMGVYVNSTSYF---ANESDAKLASQVYFKGSTVLTIPYSGNVERLQNAAG 119

QY 119 NLRNIELGNGLPEEAISALVYVYTGTTQPLTLARSFICIQMISEAARFOYIEGEMRT 178  
Db 120 KIREKIPGLFRALDSALTSIFHYDS-----TAAAFVILQTTAEASRFKIEGQIIER 174

QY 179 IRYN 182  
Db 175 IPKN 178

RESULT 14  
S22494  
rRNA N-glycosidase (EC 3.2.2.22) alpha-luffin precursor - smooth loofah  
N;Alternate names: protein synthesis inhibitor; ribosome-inactivating protein luffin-A  
C;Species: Luffa cylindrica (smooth loofah)  
C;Date: 12-Feb-1993 #sequence revision 12-Feb-1993 #text\_change 20-Aug-1999  
C;Accession: S22494; S26390; JH0202; A32542  
R;Xataoka, J.; Habuka, N.; Miyano, M.; Masuta, C.; Koiwai, A.  
Plant Mol. Biol. 18, 1199-1202, 1992  
A;Title: Nucleotide sequence of cDNA encoding alpha-luffin, a ribosome-inactivating protein  
A;Reference number: S22494; MUID:92288316; PMID:1600156  
A;Accession: S22494  
A;Molecule type: mRNA  
A;Residues: 1-277 <RAT>  
A;Cross-references: EMBL:X62371; NID:gl9145; PIDN:CAA44229.1; PID:gl9146  
R;Islam, M.R.; Nishida, H.; Funatsu, G.  
Agric. Biol. Chem. 54, 2967-2978, 1990  
A;Title: Complete amino acid sequence of luffin-a, a ribosome-inactivating protein from  
A;Reference number: S26390; MUID:91248471; PMID:1368651  
A;Accession: S26390  
A;Molecule type: protein  
A;Residues: 21-53, 'L', 55, 'I', 57-86, 'SQL', 90-154, 'L', 156-157, 'I', 159-173, 'L', 175-209, 'SL'  
R;Islam, M.R.; Nishida, H.; Funatsu, G.  
Agric. Biol. Chem. 54, 1343-1345, 1990  
A;Title: Complete amino acid sequence of luffin-a, a ribosome-inactivating protein from  
A;Reference number: JH0202; MUID:91197482; PMID:1368623  
A;Accession: JH0202  
A;Molecule type: protein  
A;Residues: 21-53, 'L', 55, 'I', 57-86, 'SQL', 90-154, 'L', 156-157, 'I', 159-173, 'L', 175-209, 'SL'  
R;Ramakrishnan, S.; Enghlid, J.J.; Bryant Jr., H.L.; Xu, F.J.  
Biochem. Biophys. Res. Commun. 160, 509-516, 1989  
A;Title: Characterization of a translation inhibitory protein from Luffa aegyptiaca.  
A;Reference number: A32542; MUID:89246493; PMID:2719679  
A;Accession: A32542  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 21-28, 'G', 30, 'X', 32-34, 'K', 36-40 <RAM>

C;Function:  
A;Description: hydrolyzes the N-glycosidic bond of a specific adenosine in 28S rRNA then  
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology  
C;Keywords: glycoprotein; glycosidase; hydrolase; seed; toxin  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-267/Product: rRNA N-glycosidase alpha-luffin #status experimental <MAT>  
F;24-262/Domain: rRNA N-glycosidase homology <RNG>  
F;268-277/Domain: carboxyl-terminal propeptide #status predicted <CTP>  
F;48,53,97,104,225,246/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F;90,179,182/Active site: Tyr, Glu, Arg #status predicted

Query Match 29.0%; Score 276; DB 2; Length 277;  
Best Local Similarity 33.3%; Pred. No. 5.7e-18;  
Matches 62; Conservative 42; Mismatches 62; Indels 20; Gaps 4;

QY 9 INFTAGATVQSYTNFIRAVRGLNTRVGLPIN-----ORFILVELSNHAEISV 57  
Db 22 VFSLSGSSSTYSKFIQDLRKALPSN-GTVYNTILLSSASGASRYTILMTLSNYDGKAI 80

QY 58 TLALDVTNAYVVGYPAGNSAYFFHPDNOEDAEATHLFTDQVNRYPFAGGNYDRLEQLA 117  
Db 81 TVAVDVTNVYMGVYVNSTSYF---NESDAKLASQYVFKGSTIVTLTPYSGNYEKLOTTAA 137

QY 118 NLRNIELGNGLPEEAISALVYVYTGTTQPLTLARSFICIQMISEAARFOYIEGEMRT 177  
Db 138 GKIREKIPGLFRALDSALTSIFHYDS-----TAAAFVILQTTAEASRFKIEGQIIIE 192

QY 178 RIRYNR 183  
Db 193 RISKNQ 198

RESULT 15  
PD0018  
mistletoe lectin I A chain - Viscum album (fragment)  
C;Species: Viscum album  
C;Date: 03-Jul-1998 #sequence\_revision 10-Jul-1998 #text\_change 26-Aug-1999  
C;Accession: PD0018  
R;Eschenburg, S.; Krauspenhaar, R.; Mikhailov, A.; Stoeva, S.; Betzel, C.; Voelter, W.  
Biochem. Biophys. Res. Commun. 247, 367-372, 1998  
A;Title: Primary structure and molecular modeling of mistletoe lectin I from Viscum album  
A;Reference number: PD0018; MUID:98308123; PMID:9642133  
A;Accession: PD0018  
A;Molecule type: protein  
A;Residues: 1-254 <ESC>  
C;Superfamily: ricin; rRNA N-glycosidase homology  
F;7-246/Domain: rRNA N-glycosidase homology <RNG>

Query Match 28.7%; Score 272.5; DB 2; Length 254;  
Best Local Similarity 37.8%; Pred. No. 1.1e-17;  
Matches 79; Conservative 30; Mismatches 53; Indels 47; Gaps 10;

QY 13 TAGATVQSYTNFIRAVR-----GRLTNRYGL-----PIN--ORFILVELSNHAEISVTL 59  
Db 9 THQTGEEYFRFTLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNGQDSVTA 68

QY 60 ALDVTNAYVVGYPAGNSAYFFHPDNOEDAEATHLFTDQVNRYPFAGGNYDRLEQLAGN 119  
Db 69 AIDVTNAYVYVAYQAGDQSYFLR-DAPRGAE--THLFTGT-TRSLPFGSSYPOLERYAGH 124

QY 120 LRENIELGNGLPEEAISALVYVYTGTTQPLTLARSFICIQMISEAARF-----QYI 171  
Db 125 -RQIPLIGDILQSVTLARF---PGSFTQARSILILQIMISEAARFNPILWRVQYI 180

QY 172 E-----GEMTRIRYN 182  
Db 181 NSGASFLPDVYVYMLELTSWGQSQSTQVQHS 209

Search completed: February 10, 2004, 16:28:03  
Job time : 11.0111 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:13:55; Search time 6.17124 Seconds  
(without alignments)  
1409.756 Million cell updates/sec

Title: US-10-083-336A-9

Perfect score: 951

Sequence: 1 IFPKQYPIINFATTAGATVQS.....ARFQVIEGEMTRIRYNRRS 185

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	934.5	98.3	576	1	RICI_RICCO
2	845	88.9	564	1	AGGL_RICCO
3	337.5	35.5	289	1	RIP1_TRIKI
4	327.5	34.4	289	1	RIPS_TRIKI
5	317	33.3	562	1	ABRC_ABRPR
6	316.5	33.3	527	1	ABRB_ABRPR
7	312	32.8	282	1	RIP2_BRVDI
8	306	32.2	563	1	NIGB_SAMNI
9	300.5	31.6	290	1	RIP1_BRVDI
10	291	30.6	528	1	ABRA_ABRPR
11	290	30.5	250	1	RIPB_LUFY
12	283	29.8	286	1	RIP1_CUCFI
13	276	29.0	277	1	RIPA_LUFY
14	272.5	28.7	254	1	MLA_VISAL
15	270.5	28.4	286	1	RIP1_MOMCH
16	268.5	28.2	286	1	RIP2_MOMBA
17	253.5	26.7	294	1	RIP1_TRIAN
18	239	25.1	316	1	RIPG_GELMU
19	184	19.3	294	1	RIPA_PHYAM
20	177.5	18.7	278	1	RIP1_MIRTA
21	169.5	17.7	313	1	RIP1_PHYAM
22	167	17.6	261	1	RIPS_PHYAM
23	131.5	13.8	253	1	RIP5_SAPOF
24	127.5	13.4	253	1	RIP2_PHYAM
25	125.5	13.2	310	1	RIP6_SAPOF
26	124.5	13.1	299	1	RIP0_DIACA
27	124	13.0	293	1	RIP2_SAPOF
28	121.5	12.8	292	1	RIP2_SAPOF
29	115.5	12.1	280	1	RIP2_HORVU
30	110	11.6	236	1	RIP3_SAPOF
31	109.5	11.5	319	1	SLTA_BP933
32	108.5	11.4	280	1	RIP1_HORVU
33	100	10.5	300	1	RIP3_MAIZE

## RESULT 1

ID	RICI_RICCO	STANDARD;	PRT;	576 AA.
AC	P02879; P02880;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Ricin precursor [Contains: Ricin A chain (xRNA N-glycosidase) (EC 3.2.2.22); Ricin B chain].			
OS	Ricinus communis (Castor bean).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eurosidia I; Malpighiales; Euphorbiaceae; Ricinus.			
OX	NCBI_TaxID=3988;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86067214; PubMed=2999712;			
RA	Halling K.C., Halling A.C., Murray E.B., Ladin B.F., Houston L.L.,			
RA	Weaver R.F.;			
RT	"Genomic cloning and characterization of a ricin gene from Ricinus			
RT	communis.";			
RL	Nucleic Acids Res. 13:8019-8033(1985).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92163016; PubMed=1371405;			
RA	Tregear J.W., Roberts L.M.;			
RT	"The lectin gene family of Ricinus communis: cloning of a functional			
RT	ricin gene and three lectin pseudogenes.";			
RL	Plant Mol. Biol. 18:515-525(1992).			
RN	[3]			
RP	SEQUENCE OF 12-576 FROM N.A.			
RX	MEDLINE=85179479; PubMed=3838723;			
RA	Lamb A., Roberts L.M., Lord J.M.;			
RT	"Nucleotide sequence of cloned cDNA coding for preproricin.";			
RL	Eur. J. Biochem. 148:265-270(1985).			
RN	[4]			
RP	SEQUENCE OF 36-302.			
RA	Yoshitake S., Funatsu G., Funatsu M.;			
RT	"Isolation and sequences of peptic peptides, and the complete			
RT	sequence of Ile chain of ricin-D.";			
RL	Agric. Biol. Chem. 42:1267-1274(1978).			
RN	[5]			
RP	SEQUENCE OF 315-576.			
RA	Funatsu G., Kimura M., Funatsu M.;			
RT	"Primary structure of Ala chain of ricin D.";			
RL	Agric. Biol. Chem. 43:2221-2224(1979).			
RN	[6]			
RP	CARBOHYDRATE-LINKAGE SITES, AND PARTIAL SEQUENCE.			
RX	MEDLINE=90344223; PubMed=1368517;			
RA	Kimura Y., Kusuoku H., Tada M., Takagi S., Funatsu G.;			
RT	"Structural analyses of sugar chains from ricin A-chain variant.";			
RL	Agric. Biol. Chem. 54:157-162(1990).			
RN	[7]			
RP	REVIEW.			
RX	MEDLINE=21480122; PubMed=11595634;			
RA	Olsnes S., Kozlov J.V.;			

P28522 zea mays (m)  
P25892 zea mays (m)  
P08026 bacterioph  
P10149 bacterioph  
Q00531 hordeum vul  
O67411 aquifex aeo  
P75255 mycoplasma  
Q943k0 erwinia chr  
Q00971 vibrio prot  
P27561 saponaria o  
P44755 haemophilus  
Q917z1 vibrio prot

## ALIGNMENTS

RT "Ricin.";  
RL Toxicon 39:1723-1728 (2001).  
RN [8]  
RX X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).  
RP MEDLINE=87165983; PubMed=3558397;  
RA Monfort W., Villafraña J.E., Monzingo A.F., Ernst S.R., Katzin B.,  
RA Rutenber E., Xuong N.H., Hamlin R., Robertus J.D.;  
RT "The three-dimensional structure of ricin at 2.8 Å.";  
RL J. Biol. Chem. 262:5398-5403 (1987).  
RN [9]  
RX X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.  
RP MEDLINE=91352004; PubMed=1881881;  
RA Katzin B.J., Collins E.J., Robertus J.D.;  
RT "Structure of ricin A-chain at 2.5 Å.";  
RL Proteins 10:251-259 (1991).  
RN [10]  
RX X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF B-CHAIN.  
RP MEDLINE=91352005; PubMed=1881882;  
RA Rutenber E., Robertus J.D.;  
RT "Structure of ricin B-chain at 2.5-Å resolution.";  
RL Proteins 10:260-269 (1991).  
RN [11]  
RX X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF A-CHAIN.  
RP MEDLINE=95082010; PubMed=7990130;  
RA Weston S.A., Tucker A.D., Thatcher D.R., Derbyshire D.J.,  
RA Paupit R.A.;  
RT "X-ray structure of recombinant ricin A-chain at 1.8-Å resolution.";  
RL J. Mol. Biol. 244:410-422 (1994).  
RN [12]  
RX X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT HIS-215.  
RP MEDLINE=96374222; PubMed=8780513;  
RA Day P.J., Ernst S.R., Frankel A.E., Monzingo A.F., Pascal J.M.,  
RA Molina-Svinth M.C., Robertus J.D.;  
RT "Structure and activity of an active site substitution of ricin A chain.";  
RL Biochemistry 35:11098-11103 (1996).  
RN [13]  
RX X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.  
RP MEDLINE=97240820; PubMed=9086280;  
RA Yan X., Hollis T., Svinth M., Day P., Monzingo A.F., Milne G.W.,  
RA Robertus J.D.;  
RT "Structure-based identification of a ricin inhibitor.";  
RL J. Mol. Biol. 266:1043-1049 (1997).  
RN [14]  
RX MUTAGENESIS.  
RP MEDLINE=93165632; PubMed=1287657;  
RA Kin Y., Robertus J.D.;  
RT "Analysis of several key active site residues of ricin A chain by mutagenesis and X-ray crystallography.";  
RL Protein Eng. 5:775-779 (1992).  
CC -!- FUNCTION: Ricin is highly toxic to animal cells and to a less extent to plant cells. The A chain is responsible for inhibiting protein synthesis through the catalytic inactivation of 60S ribosomal subunits. It acts as a glycosidase that removes a specific adenine residue from an exposed loop of 28S ribosomal RNA. As this loop is involved in the binding of elongation factors, the modified ribosomes are unable to support protein synthesis. The A chain can inactivate a few thousand ribosomes per minute, thus inactivating them faster than the cell can make new ones. A single A-chain molecule can therefore kill an animal cell. The B chain binds to cell receptors and facilitates the entry into the cell of the A chain; B chains are also responsible for cell agglutination (lectin activity). It binds to beta-D-galactopyranoside moieties.  
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.  
CC -!- SUBUNIT: Disulfide-linked dimer of A and B chains.  
CC -!- DOMAIN: The B chain is composed of two domains, each domain consists of 3 homologous subdomains (alpha, beta, gamma).  
CC -!- PTM: THE MAJOR A-CHAIN IS GLYCOSYLATED ONLY IN POSITION 45 AND THE MINOR A-CHAIN IS GLYCOSYLATED ALSO IN POSITION 271.  
CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.

CC -!- SIMILARITY: Contains 2 ricin B-type lectin domains.  
CC -!- CAUTION: REF.4 AND REF.5 SEQUENCES HAVE A HIGH NUMBER OF CONFLICTS WITH THE SEQUENCE TRANSLATED FROM DNA (REF.1, REF.2 AND REF.3).  
CC -!- DATABASE: NAME-Protein Spotlight;  
CC NOTE-Issue 31 of February 2003;  
CC WWW=http://www.expasy.org/spotlight/articles/sptlt031.html".  
CC -----  
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CC -----  
CC EMBL; X03179; CAA26393.1; -;  
CC EMBL; X52908; CAA37095.1; -;  
CC EMBL; X02388; CAA26230.1; -;  
CC EMBL; A12892; CAA01058.1; -;  
CC PIR; A24041; RLCSO.  
CC PDB; 2AAL; 31-JAN-94.  
CC PDB; 1APG; 31-JAN-94.  
CC PDB; 1FMP; 31-OCT-93.  
CC PDB; 1IFS; 14-JAN-98.  
CC PDB; 1IFT; 14-JAN-98.  
CC PDB; 1IFU; 14-JAN-98.  
CC PDB; 1ITC; 31-OCT-93.  
CC PDB; 1OBS; 16-JUN-97.  
CC PDB; 1OBT; 16-JUN-97.  
CC PDB; 1BR5; 02-SEP-98.  
CC PDB; 1BR6; 02-SEP-98.  
CC PDB; 1IL3; 16-JAN-02.  
CC PDB; 1IL4; 16-JAN-02.  
CC PDB; 1IL9; 16-JAN-02.  
CC GlycoSuiteDB; P02879; -;  
CC InterPro; IPR000772; Ricin\_B\_lectin.  
CC InterPro; IPR001574; RIP.  
CC Pfam; PF00652; Ricin\_B\_lectin; 6.  
CC Pfam; PF00161; RIP; 1.  
CC PRINTS; PR00396; SHIGARICIN.  
CC SMART; SM00458; RICIN; 2.  
CC PROSITE; PS0231; RICIN\_B\_LECTIN; 2.  
CC PROSITE; PS00275; SHIGA\_RICIN; 1.  
CC Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;  
KW Glycoprotein; Lectin; Signal; 3D-structure.  
FT SIGNAL 1 35  
FT CHAIN 36 302  
FT PEPTIDE 303 314  
FT CHAIN 315 576  
FT DOMAIN 321 448  
FT DOMAIN 451 575  
FT REPEAT 331 373  
FT REPEAT 374 414  
FT REPEAT 417 449  
FT REPEAT 462 497  
FT REPEAT 501 540  
FT REPEAT 543 570  
FT ACT\_SITE 212 212  
FT DISULFID 294 318  
FT DISULFID 334 353  
FT DISULFID 377 394  
FT DISULFID 465 478  
FT DISULFID 504 521  
FT CARBOHYD 45 45  
FT CARBOHYD 271 271  
FT CARBOHYD 409 409  
FT CARBOHYD 449 449  
FT CONFLICT 76 76  
FT CONFLICT 551 551  
FT STRAND 43 47  
FT TURN 49 50  
FT N-LINKED (GLCNAC. . .).  
FT /FTID-CAR 000080. . . (IN MINOR FORM).  
FT N-LINKED (GLCNAC. . .).  
FT /FTID-CAR 000081. . .  
FT N-LINKED (GLCNAC. . .).  
FT N-LINKED (GLCNAC. . .).  
FT E -> D (IN REF. 3).  
FT CONFLICT 551 551  
FT STRAND 43 47  
FT TURN 49 50

Query Match 98.3%; Score 934.5; DB 1; Length 576;  
 Best Local Similarity 93.4%; Pred. No. 6.9e-80;  
 Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 IFFKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINORFV 47  
 DB 36 IFFKQYPIINFTTAGATVQSYTNFIRAVRGRLTGDVDRHEIPVLPNRVGLPINORFV 95

QY 48 ELSNHAELSVTLALDVTNAVVGVRAGNSAYFFHPDQEDAEATHTLFTDVQNYRTFAFG 107  
 DB 96 ELSNHAELSVTLALDVTNAVVGVRAGNSAYFFHPDQEDAEATHTLFTDVQNYRTFAFG 155

QY 108 GNYDRLEQLAGNLRNLELNGPLERAEISALYYSTGTQPLTLARSFFIICIMISEAR 167  
 DB 156 GNYDRLEQLAGNLRNLELNGPLERAEISALYYSTGTQPLTLARSFFIICIMISEAR 215

QY 168 FOYIEGEMTRIRYNRRS 185  
 DB 216 FOYIEGEMTRIRYNRRS 233

RESULT 2  
 AGGL RICCO STANDARD; PRT; 564 AA.  
 ID AC P06750;  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Agglutinin precursor (RCA) [Contains: Agglutinin A chain (rRNA N-  
 DE Glycosidase) (EC 3.2.2.22); Agglutinin B chain].  
 OS Ricinus communis (Castor bean).  
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;  
 OC eurosids I; Malpighiales; Euphorbiaceae; Ricinus.  
 OX NCBI\_TaxID=3988;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=86059449; PubMed=2999130;  
 RA Roberts L.M., Lamb F.I., Pappin D.J.C., Lord J.M.;  
 RT "The primary sequence of Ricinus communis agglutinin. Comparison with  
 RL ricin."; Chem. 260:15682-15686(1985).  
 [2]  
 RN SEQUENCE OF 303-564.  
 RX TISSUE=Seed;  
 RA Araki T., Yoshioka Y., Funatsu G.;  
 RT "The complete amino acid sequence of the B-chain of the Ricinus  
 RL communis agglutinin isolated from large-grain castor bean seeds.";  
 RL Biochim. Biophys. Acta 872:277-285(1986).  
 [3]  
 RN SEQUENCE OF 303-337.  
 RX MEDLINE=80178723; PubMed=6768555;  
 RA Lin T.-S., Li S.-L.;  
 RT "Purification and physicochemical properties of ricins and  
 RL agglutinins from Ricinus communis.";  
 RL Eur. J. Biochem. 105:453-459(1980).  
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 CC specific adenosine on the 28S rRNA.  
 CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-  
 CC INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUPERFAMILY.  
 CC -!- SIMILARITY: Contains 2 ricin B-type lectin domains.  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL; M12089; AAA33869.1; -;  
 CC EMBL; S40368; AAB22584.1; -;

PIR; A24261; RLCSAG.  
 DR HSP; P02879; IBrE.  
 DR GlycoSuitedB; P06750; -;  
 DR InterPro; IPR000772; Ricin\_B\_lectin.  
 DR InterPro; IPR001574; RIP.  
 DR Pfam; PF00652; Ricin\_B\_lectin; 6.  
 DR Pfam; PF00161; RIP; 1.  
 DR PRINTS; P00396; SHIGARICIN.  
 DR SMART; SM00458; RICIN; 2.  
 DR PROSITE; PS00231; RICIN\_B\_LECTIN; 2.  
 DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
 KW Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;  
 KW Glycoprotein; Lectin; Signal.  
 FT SIGNAL 1 24 POTENTIAL.  
 FT CHAIN 25 290 AGGLUTININ A CHAIN.  
 FT PROPEP 291 302 LINKER PEPTIDE.  
 FT CHAIN 303 564 AGGLUTININ B CHAIN.  
 FT DOMAIN 309 436 RICIN B-TYPE LECTIN 1.  
 FT DOMAIN 439 563 RICIN B-TYPE LECTIN 2.  
 FT REPEAT 319 361 1-ALPHA.  
 FT REPEAT 362 402 1-BETA.  
 FT REPEAT 403 437 1-GAMMA.  
 FT REPEAT 450 485 2-ALPHA.  
 FT REPEAT 489 528 2-BETA.  
 FT REPEAT 531 558 2-GAMMA.  
 FT ACT\_SITE 200 200 BY SIMILARITY.  
 FT DISULFID 282 306 INTERCHAIN (BY SIMILARITY).  
 FT DISULFID 322 341 BY SIMILARITY.  
 FT DISULFID 365 382 BY SIMILARITY.  
 FT DISULFID 453 466 BY SIMILARITY.  
 FT DISULFID 492 509 BY SIMILARITY.  
 FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 437 437 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 331 331 F -> T (IN REF. 2).  
 FT CONFLICT 362 362 N -> D (IN REF. 2).  
 FT CONFLICT 374 374 R -> G (IN REF. 2).  
 FT CONFLICT 404 404 R -> T (IN REF. 2).  
 FT CONFLICT 552 552 F -> V (IN REF. 2).  
 SQ SEQUENCE 564 AA; 62851 MW; D455F2A72F609759 CRC64;

Query Match 88.9%; Score 845; DB 1; Length 564;  
 Best Local Similarity 85.4%; Pred. No. 1.6e-71;  
 Matches 169; Conservative 7; Mismatches 8; Indels 14; Gaps 2;

QY 1 IFFKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINORFV 47  
 DB 25 IFFKQYPIINFTTAGATVQSYTNFIRAVRGRLTGDVDRHEIPVLPNRVGLPINORFV 84

QY 48 ELSNHAELSVTLALDVTNAVVGVRAGNSAYFFHPDQEDAEATHTLFTDVQNYRTFAFG 107  
 DB 85 ELSNHAELSVTLALDVTNAVVGVRAGNSAYFFHPDQEDAEATHTLFTDVQNYRTFAFG 144

QY 108 GNYDRLEQLAGNLRNLELNGPLERAEISALYYSTGTQPLTLARSFFIICIMISEAR 167  
 DB 145 GNYDRLEQLAGNLRNLELNGPLERAEISALYYSTGTQPLTLARSFFIICIMISEAR 203

QY 168 FOYIEGEMTRIRYNRRS 185  
 DB 204 FOYIEGEMTRIRYNRRS 221

RESULT 3  
 RIPT TRIKI STANDARD; PRT; 289 AA.  
 ID RIPT TRIKI  
 AC P09989;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ribosome-inactivating protein alpha-trichosanthin precursor  
 DE (rRNA N-glycosidase) (EC 3.2.2.22) (Alpha-TCS).  
 OS Trichosanthes kirilowii (Mongolian snake-gourd).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.  
 OX NCBI\_TaxID=3677;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RP STRAIN=Maximowicz;  
 RP MEDLINE=91153657; PubMed=1999291;  
 RA Shaw P.C., Yung M.H., Zhu R.H., Ho W.K.K., Ng T.B., Yeung H.W.;  
 RA "Cloning of trichosanthin cDNA and its expression in *Escherichia*  
 RT *coli*.";   
 RL Gene 97:267-272 (1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RP STRAIN=Maximowicz; TISSUE=Leaf;  
 RP MEDLINE=90256790; PubMed=2341400;  
 RA Chow T., Feldman R.A., Lovett M., Piatak M.;  
 RA "Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a  
 RT type I ribosome-inactivating protein.";   
 RL J. Biol. Chem. 265:8670-8674 (1990).  
 RN [3]  
 RP SEQUENCE OF 24-270.  
 RP STRAIN=Maximowicz; TISSUE=Tubercous root;  
 RA Collins E.J., Robertus J.D., Lopresti M., Stone K.L., Williams K.R.,  
 RA Wu P., Hwang K., Piatak M.;  
 RA "Primary amino acid sequence of alpha-trichosanthin and molecular  
 RT models for abrin A-chain and alpha-trichosanthin.";   
 RL J. Biol. Chem. 265:8665-8669 (1990).  
 RN [4]  
 RP SEQUENCE OF 24-270.  
 RP TISSUE=Tubercous root;  
 RA Wang Y., Qian R.Q., Gu Z.W., Jin S.W., Zhang L.Q., Xia Z.X.,  
 RA Tian G.Y., Ni C.Z.;  
 RA "Scientific evaluation of Tian Hua Fen (THF): history, chemistry and  
 RT application.";   
 RL Pure Appl. Chem. 58:789-798 (1986).  
 RN [5]  
 RP X-RAY CRYSTALLOGRAPHY (1.88 ANGSTROMS).  
 RP MEDLINE=94344957; PubMed=8066085;  
 RA Zhou F., Fu Z., Chen M., Lin Y., Pan K.;  
 RA "Structure of trichosanthin at 1.88-A resolution.";   
 RL Proteins 19:4-13 (1994).  
 RN [6]  
 RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).  
 RP MEDLINE=95344383; PubMed=7619070;  
 RA Huang Q., Liu S., Tang Y., Jin S., Wang Y.;  
 RA "Studies on crystal structures, active-centre geometry and  
 RT depurinating mechanism of two ribosome-inactivating proteins.";   
 RL Biochem. J. 309:285-298 (1995).  
 CC -!- FUNCTION: TRICHOSANTHIN IS AN ABORTION-INDUCING PROTEIN. IT IS  
 CC CAPABLE OF INHIBITING HIV-1 INFECTION AND REPLICATION. IT  
 CC INACTIVATES EUKARYOTIC 60S RIBOSOMAL SUBUNITS.  
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 CC specific adenosine on the 28S rRNA.  
 CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC TYPE 1 RIP SUBFAMILY.  
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 CC -----  
 DR EMBL; M34858; AAA34207.1; -;  
 DR EMBL; J05434; AAA34206.1; -;  
 DR PIR; J05666; RLTZT.  
 DR PDB; 1MRJ; 07-FEB-95.  
 DR PDB; 1MRK; 07-FEB-95.  
 DR PDB; 1TCS; 10-JUL-95.  
 DR PDB; 1J4G; 28-JAN-03.

DR PDB; 1NLI; 21-JAN-03.  
 DR PDB; 1QD2; 24-APR-00.  
 DR InterPro; IPR001574; RIP.  
 DR Pfam; PF00161; RIP; 1.  
 DR PRINTS; PR00396; SHIGARICIN.  
 DR PROSITE; PS00275; SHIGA RICHIN; 1.  
 KW Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;  
 KW Toxin; Signal; 3D-structure.  
 FT SIGNAL 1 23  
 FT CHAIN 24 270  
 FT  
 FT PROPEP 271 289  
 FT ACT SITE 183 183  
 FT CONFLICT 57 60  
 FT CONFLICT 82 84  
 FT CONFLICT 87 87  
 FT CONFLICT 92 92  
 FT CONFLICT 143 144  
 FT CONFLICT 196 196  
 FT CONFLICT 215 216  
 FT CONFLICT 231 231  
 FT CONFLICT 234 234  
 FT CONFLICT 246 266  
 FT CONFLICT 247 247  
 FT STRAND 25 28  
 FT TURN 30 31  
 FT HELIX 34 46  
 FT TURN 47 47  
 FT STRAND 50 54  
 FT TURN 55 56  
 FT STRAND 57 60  
 FT HELIX 66 69  
 FT STRAND 70 76  
 FT TURN 78 79  
 FT STRAND 82 88  
 FT TURN 89 92  
 FT STRAND 93 99  
 FT TURN 100 101  
 FT STRAND 102 105  
 FT HELIX 109 114  
 FT TURN 115 117  
 FT TURN 120 121  
 FT STRAND 124 127  
 FT HELIX 134 141  
 FT TURN 142 142  
 FT HELIX 145 147  
 FT STRAND 150 150  
 FT HELIX 152 163  
 FT TURN 164 165  
 FT HELIX 167 180  
 FT TURN 181 181  
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 FT TURN 241 242  
 FT STRAND 245 250  
 FT TURN 251 252  
 FT HELIX 254 258  
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 FT STRAND 260 260  
 FT TURN 263 263  
 FT TURN 266 268  
 SQ SEQUENCE 289 AA; 31676 MW; 5CE09BB630575BB9 CRC64;  
 Query Match 35.5%; Score 337.5; DB 1; Length 289;  
 Best Local Similarity 39.0%; Pred. No. 2.2e-24;  
 Matches 71; Conservative 42; Mismatches 50; Indels 19; Gaps 4;



MEDLINE=93132798; PubMed=8421131;  
 Hung C.-H., Lee M.-C., Lee T.C., Lin J.-Y.;  
 "Primary structure of three distinct isoforms determined by cDNA  
 sequencing. Conservation and significance.";  
 J. Mol. Biol. 229:263-267(1993).  
 [2]  
 SEQUENCE OF 260-527.  
 TISSUE=Seed;  
 MEDLINE=93169023; PubMed=7763422;  
 Kimura M., Sumizawa T., Funatsu G.;  
 "The complete amino acid sequences of the B-chains of abrin-a and  
 abrin-b, toxic proteins from the seeds of Abrus precatorius.";  
 Biosci. Biotechnol. Biochem. 57:166-169(1993).  
 CC !- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN  
 CC SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL  
 CC SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA.  
 CC ABRIN-A IS MORE TOXIC THAN RICIN.  
 CC !- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT  
 CC FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT  
 CC PRECEDES ENDOCYTOSIS.  
 CC !- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 CC specific adenosine on the 28S rRNA.  
 CC !- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.  
 CC !- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN  
 CC CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).  
 CC !- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-  
 CC INACTIVATING PROTEIN FAMILY, TYPE 2 RIP SUBFAMILY.  
 CC !- SIMILARITY: Contains 2 ricin B-type lectin domains.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; M98345; AAA32625.1; -;  
 CC PIR; S32430; S32430.  
 CC HSPSP; P11140; LABR.  
 CC InterPro; IPR000772; Ricin\_B\_lectin.  
 CC InterPro; IPR001574; RIP.  
 CC Pfam; PF00652; Ricin\_B\_lectin; 6.  
 CC Pfam; PF00161; RIP; 1.  
 CC PRINTS; PR00396; SHIGARICIN.  
 CC SMART; SM00458; RICIN; 2.  
 CC PROSITE; PS50231; RICIN\_B\_LECTIN; 2.  
 CC PROSITE; PS00275; SHIGA\_RICIN; 1.  
 CC Plant defense; Hydrolyase; Protein synthesis inhibitor; Toxin; Repeat;  
 CC Glycoprotein; lectin; Pyrrolidone carboxylic acid.  
 CC CHAIN 1 250 ABRIN-B A CHAIN.  
 CC PEPTIDE 251 260 LINKER PEPTIDE.  
 CC CHAIN 261 527 ABRIN-B B CHAIN.  
 CC DOMAIN 272 399 RICIN B-TYPE LECTIN 1.  
 CC DOMAIN 402 526 RICIN B-TYPE LECTIN 2.  
 CC REPEAT 282 324 1-ALPHA.  
 CC REPEAT 325 365 1-BETA.  
 CC REPEAT 368 400 1-GAMMA.  
 CC REPEAT 413 448 2-ALPHA.  
 CC REPEAT 452 491 2-BETA.  
 CC REPEAT 494 527 2-GAMMA.  
 CC ACT SITE 163 163 BY SIMILARITY.  
 CC DISULFID 246 268 INTERCHAIN (BY SIMILARITY).  
 CC DISULFID 285 304 BY SIMILARITY.  
 CC DISULFID 328 345 BY SIMILARITY.  
 CC DISULFID 416 429 BY SIMILARITY.  
 CC DISULFID 455 472 BY SIMILARITY.  
 CC MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID (BY  
 CC SIMILARITY).  
 CC CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CONFLICT 282 282 N -> D (IN REF. 2).  
 CC

FT 291 291 D -> N (IN REF. 2).

FT 350 351 AE -> PQ (IN REF. 2).

FT 378 378 S -> N (IN REF. 2).

FT 426 426 L -> M (IN REF. 2).

FT 428 428 Y -> D (IN REF. 2).

FT 431 431 N -> S (IN REF. 2).

FT 431 431 R -> K (IN REF. 2).

FT 484 484 N -> S (IN REF. 2).

FT 491 491 H -> Y (IN REF. 2).

FT 493 493 R -> G (IN REF. 2).

FT 502 502 E -> Q (IN REF. 2).

FT 509 509 H -> Q (IN REF. 2).

FT 513 513 H -> T (IN REF. 2).

FT 516 516 H -> T (IN REF. 2).

SQ SEQUENCE 527 AA; 59114 MW; 3253AE490CE9494A CRC64;

Query Match 33.3%; Score 316.5; DB 1; Length 527;

Best Local Similarity 42.9%; Pred. No. 4.3e-22;

Matches 81; Conservative 23; Mismatches 66; Indels 19; Gaps 5;

QY 5 QYPIINFTAGATVQSYTFIRAVRGLNRYV--GLPI-----NORFILVELSNEA 53

DB 1 QDQVIFTEGATSQSYKQFIEALRQLRGLHGPVLPDPPTLQERNRYISVELNSD 60

QY 54 ELSVTLALDVTNAYVGVYRAGNSAYFFHPDQDAEAIHLFTDQVNRVTFAGGNYDRL 113

DB 61 TSEIAGIDVSNAYVAYRAGNSYFL--RDAPTSASRYLFTGTQ-QYSLRENGSYIDL 116

QY 114 EQLAGNLRENIELGNGPLERALSALYYTGGTQPLTARSFICITOMISEAARFOYIEG 173

DB 117 ERLARTRQIQIPLGLQALRHAIISFL---QSGTDDQEIARTLIVTIQMASAARYRFISY 172

QY 174 EMETRYRN 182

DB 173 RGVGSIRTN 181

RESULT 7

RIP2\_BRYDI STANDARD; PRT; 282 AA.

AC P98184; Q9S8J0;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Ribosome-inactivating protein bryodin II precursor (rRNA N-glycosidase) (EC 3.2.2.22) (SD2).

OS Bryonia dioica (Red bryonia).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eucosids 1; Cucurbitales; Cucurbitaceae; Bryonia.

OX NCBI\_TaxID=3652;

RN [1]

RP SEQUENCE FROM N.A.

RA Siegal C.B., Gawlak S.L., Marquardt H.;

RT "Bryodin 2 a ribosome-inactivating protein isolated from the plant Bryonia dioica.";

RL Patent number US5597569, 28-JAN-1997.

RN [2]

RP SEQUENCE OF 22-42.

RC TISSUE=Root;

RX MEDLINE=95151812; PubMed=7849072;

RA Siegal C.B., Gawlak S.L., Chace D., Wolff E.A., Mixan B., Marquardt H.;

RT "Characterization of ribosome-inactivating proteins isolated from Bryonia dioica and their utility as carcinoma-reactive immunoconjugates.";

RL Bioconj. Chem. 5:423-429(1994).

CC -!- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS PROTEIN SYNTHESIS IN ANIMAL CELLS (BY SIMILARITY).

CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.

CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 1 RIP SUBFAMILY.

CC -!- FUNCTION: NON-TOXIC TYPE 2 RIP WHICH STRONGLY INHIBITS MAMMALIAN

CC

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CC

DR EMBL; I34238; -; NOT\_ANNOTATED\_CDS.

DR HSSP; P09989; IMR9.

DR InterPro; IPR001574; RIP.

DR Pfam; PF00161; RIP; 1.

DR PRINTS; PR00396; SHIGARICIN.

DR PROSITE; PS00275; SHIGA\_RICIN; 1.

KW Plant defense; Protein synthesis inhibitor; Hydrolyase; Toxin;

KW Multigene family; Glycoprotein; Signal.

FT SIGNAL 1 21 RIBOSOME-INACTIVATING PROTEIN BRYODIN II.

FT CHAIN 22 282 BY SIMILARITY.

FT ACT SITE 183 183 N-LINKED (GLCNAC... ) (POTENTIAL).

FT CARBOHYD 25 25

SQ SEQUENCE 282 AA; 30754 MW; C52BE2F6A873769C CRC64;

Query Match 32.8%; Score 312; DB 1; Length 282;

Best Local Similarity 45.5%; Pred. No. 5.3e-22;

Matches 81; Conservative 24; Mismatches 49; Indels 24; Gaps 8;

QY 9 INFTTAGATVQSYTFIRAVRGLNRYV-----LPINQ-----RFILVELSNAEL 55

DB 24 INFSIGATGATYKTFIRMLTKLT--VGTPRYDIPVLRNAAAGLARQLVLTNYNGE 81

QY 56 SVTLALDVTNAYVGVYRAGNSAYFFHPDQDAEAIHLFTDQVNRVTFAGGNYDRLSQ 115

DB 82 SVTVALDVVVVYVAYRAGNTAYFL--ADASTEANNVLFAGI-NHVRLPYGGYDGLST 137

QY 116 LAGNL-RENIELGNGPLERALSALYYTGGTQPLTARSFICITOMISEAARFOYIE 172

DB 138 AAGRISRENIELGFSISSAIGNFRHNP-GTSVP---RAFVITQTVSEAAARFKYIE 191

RESULT 8

RIP2\_SAMNI STANDARD; PRT; 563 AA.

AC P33183; P33184; P93542;

DT 01-OCT-1993 (Rel. 27, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Nigrin b precursor (Agglutinin V) (SNAV) [Contains: Nigrin b A chain (rRNA N-glycosidase) (EC 3.2.2.22); Nigrin b B chain].

OS Sambucus nigra (European elder).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; Campanulids; Dipsacales; Adoxaceae; Sambucus.

OX NCBI\_TaxID=4202;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Bark;

RX MEDLINE=96215449; PubMed=8647092;

RA Van Damme E.J., Barre A., Rouge P., Van Leuven F., Peumans W.J.;

RT "Characterization and molecular cloning of Sambucus nigra agglutinin V (nigrin b), a GalNAc-specific type-2 ribosome-inactivating protein from the bark of elderberry (Sambucus nigra).";

RL Eur. J. Biochem. 237:505-513 (1996).

RN [2]

RP SEQUENCE OF 26-49 AND 298-321.

RC TISSUE=Bark;

RX MEDLINE=94003077; PubMed=8400135;

RA Girbes T., Citores L., Ferreras J.M., Rojo M.A., Iglesias R., Munoz R., Arias F.J., Calonge M., Garcia J.R., Mendez E.;

RT "Isolation and partial characterization of nigrin b, a non-toxic novel type 2 ribosome-inactivating protein from the bark of Sambucus nigra L.";

RT nigrin L.";

RL Plant Mol. Biol. 22:1181-1186(1993).

CC -!- FUNCTION: NON-TOXIC TYPE 2 RIP WHICH STRONGLY INHIBITS MAMMALIAN

CC







CC INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.  
 CC -I- SIMILARITY: Contains 2 ricin B-type lectin domains.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; M98344; AAA32624.1; ALT INIT.  
 CC EMBL; X54872; -; NOT\_ANNOTATED\_CDS.  
 CC PIR; S32429; TZLSA.  
 CC PDB; IABR; 07-FEB-95.  
 CC InterPro; IPR000772; Ricin\_B\_lectin.  
 CC InterPro; IPR001574; RIP.  
 CC Pfam; PF00652; Ricin\_B\_lectin; 6.  
 CC Pfam; PF00161; RIP; 1.  
 CC PRINTS; PR00396; SHIGARICIN.  
 CC SMART; SM00458; RICIN; 2.  
 CC PROSITE; PS0231; RICIN\_B\_LECTIN; 2.  
 CC PROSITE; PS0275; SHIGA\_RICIN; 1.  
 CC Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;  
 CC Glycoprotein; Lectin; 3D-structure; Pyrrolidone carboxylic acid.  
 CC CHAIN 1 251 ABRIN-A A CHAIN.  
 CC PEPTIDE 252 261 LINKER PEPTIDE.  
 CC CHAIN 262 528 ABRIN-A B CHAIN.  
 CC DOMAIN 273 400 RICIN B-TYPE LECTIN 1.  
 CC DOMAIN 403 527 RICIN B-TYPE LECTIN 2.  
 CC REPEAT 283 325 1-ALPHA.  
 CC REPEAT 326 366 1-BETA.  
 CC REPEAT 369 401 1-GAMMA.  
 CC REPEAT 414 449 2-ALPHA.  
 CC REPEAT 453 492 2-BETA.  
 CC REPEAT 495 528 2-GAMMA.  
 CC ACT SITE 164 164 INTERCHAIN (BY SIMILARITY).  
 CC DISULFID 247 269 BY SIMILARITY.  
 CC DISULFID 286 305 BY SIMILARITY.  
 CC DISULFID 329 346 BY SIMILARITY.  
 CC DISULFID 417 430 BY SIMILARITY.  
 CC DISULFID 456 473 BY SIMILARITY.  
 CC MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 CC CARBOHYD 361 361 N-LINKED (GLCNAC. .).  
 CC CARBOHYD 401 401 N-LINKED (GLCNAC. .).  
 CC CONFLICT 202 202 MISSING (IN REF. 2).  
 CC CONFLICT 298 298 N -> Y (IN REF. 4).  
 CC CONFLICT 427 427 M -> L (IN REF. 4).  
 CC CONFLICT 467 467 T -> P (IN REF. 4).  
 CC CONFLICT 483 483 V -> L (IN REF. 4).  
 CC STRAND 5 8  
 CC TURN 10 11  
 CC HELIX 14 28  
 CC STRAND 32 33  
 CC TURN 34 35  
 CC STRAND 36 38  
 CC TURN 42 43  
 CC HELIX 47 49  
 CC STRAND 51 57  
 CC STRAND 63 69  
 CC TURN 70 72  
 CC STRAND 75 79  
 CC STRAND 83 86  
 CC TURN 88 89  
 CC TURN 92 93  
 CC HELIX 94 97  
 CC TURN 100 101  
 CC STRAND 103 106  
 CC TURN 113 114  
 CC TURN 115 119  
 CC TURN 124 126  
 CC STRAND 129 129  
 CC HELIX 131 142

FT TURN 143 144  
 FT HELIX 148 167  
 FT STRAND 168 168  
 FT HELIX 169 180  
 FT TURN 181 182  
 FT STRAND 185 185  
 FT HELIX 189 196  
 FT TURN 197 197  
 FT HELIX 198 207  
 FT STRAND 212 220  
 FT TURN 222 223  
 FT STRAND 226 231  
 FT TURN 232 233  
 FT HELIX 235 239  
 FT STRAND 240 240  
 FT STRAND 243 243  
 FT STRAND 248 248  
 FT STRAND 268 268  
 FT STRAND 276 277  
 FT STRAND 279 280  
 FT HELIX 282 284  
 FT STRAND 286 289  
 FT HELIX 290 292  
 FT TURN 296 297  
 FT STRAND 299 303  
 FT HELIX 311 313  
 FT STRAND 315 317  
 FT TURN 319 320  
 FT STRAND 322 325  
 FT TURN 326 327  
 FT STRAND 328 332  
 FT TURN 337 338  
 FT STRAND 340 344  
 FT TURN 346 348  
 FT HELIX 351 353  
 FT STRAND 355 355  
 FT STRAND 357 358  
 FT TURN 360 361  
 FT STRAND 364 366  
 FT TURN 367 370  
 FT STRAND 371 374  
 FT TURN 380 381  
 FT STRAND 383 383  
 FT STRAND 385 387  
 FT HELIX 393 395  
 FT STRAND 398 399  
 FT STRAND 406 408  
 FT STRAND 410 411  
 FT HELIX 413 415  
 FT STRAND 417 421  
 FT TURN 422 423  
 FT STRAND 424 428  
 FT TURN 432 433  
 FT HELIX 435 437  
 FT STRAND 439 441  
 FT TURN 443 444  
 FT STRAND 447 449  
 FT TURN 450 451  
 FT STRAND 452 459  
 FT TURN 464 465  
 FT STRAND 467 472  
 FT TURN 474 475  
 FT HELIX 478 480  
 FT STRAND 483 484  
 FT TURN 486 487  
 FT STRAND 490 492  
 FT TURN 493 496  
 FT STRAND 497 501

Query Match 30.6%; Score 291; DB 1; Length 528;  
 Best Local Similarity 40.6%; Pred. No. le-19;  
 Matches 76; Conservative 26; Mismatches 59; Indels 26; Gaps 7;

QY 9 INFTTAGATVQSYTNFIRAVRGRLTNVGL-----PI-----NQRFILVELSNHAEL 55  
 DB 5 IKFSTEGATSGYKQFIEALRERL--RGLIHIDIVLPDPTTLQERNRYITVELSNSDTE 62  
 QY 56 SYTLALDVTNAVYVGRAGNSAYFFH--PDNQEDAEATHLFTDQVNRYYTFAFGNGYDRL 113  
 DB 63 STEVGIDVTNAVYVAYRAGTQSYFLDAPSSASD-----YLFTGT-DQHSLLPFYGTGDL 116  
 QY 114 EQLAGNLRENIELGNPLEEALISALYYSTGTQTLPTLARSFIIICMISEARFOYIEG 173  
 DB 117 ERWAHQSRQIPLGLQALTHGIS----PFRSGNDNEEKARTLIVTIQWVAEAPRYISN 173  
 QY 174 EMRTIR 180  
 DB 174 RRVSIQ 180

## RESULT 11

RIPB\_LUFCV STANDARD; PRT; 250 AA.  
 AC P22851;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Ribosome-inactivating protein luffin-B (tRNA N-glycosidase)  
 DE (EC 3.2.2.22).  
 OS Luffa cylindrica (Smooth loofah) (Sponge gourd).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Cucurbitales; Cucurbitaceae; Luffa.  
 OX NCBI\_TaxID=3670;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Seed;  
 RX MEDLINE=91248488; PubMed=1368666;  
 RA Islam M.R., Hirayama H., Funatsu G.;  
 RT "Complete amino acid sequence of luffin-b, a ribosome-inactivating  
 RT protein from sponge gourd (Luffa cylindrica) seeds.";  
 RL Agric. Biol. Chem. 55:229-238(1991).  
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 CC specific adenosine on the 28S rRNA.  
 CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC TYPE 1 RIP SUBFAMILY.

DR PIR; JN0108; JN0108.  
 DR HSSP; P16094; LAHC.  
 DR InterPro; IPR001574; RIP.  
 DR Pfam; PF00161; RIP; 1.  
 DR PRINTS; PR00396; SHIGARICIN.  
 DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
 KW Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;  
 KW Toxin.  
 FT ACT SITE 160 160 BY SIMILARITY.  
 FT SEQUENCE 250 AA; 27293 MW; F01ABDC8A1078700 CRC64;

Query Match 30.5%; Score 290; DB 1; Length 250;  
 Best Local Similarity 33.2%; Pred. No. 5.2e-20;  
 Matches 61; Conservative 48; Mismatches 57; Indels 18; Gaps 4;

QY 9 INFTTAGATVQSYTNFIRAVRGRLTNR---VGLPI-----NQRFILVELSNHAELSVT 58  
 DB 3 VPSLSGADSKSYKFTALRKALPSKVSNIPLLLPSASGASRYILMLQSLNDYDAKIT 62  
 QY 59 LALDVTNAVYVGRAGNSAYFFHDPNQEDAEATHLFTDQVNRYYTFAFGNGYDRLQLAG 118  
 DB 63 MALDVTNVYIMGLVNSTSYF---ANESDAKLASQVYFKGSTVLTIPYSNYERLQNAAG 119  
 QY 119 NLRENIELGNPLEEALISALYYSTGTQTLPTLARSFIIICMISEARFOYIEGMRTR 178  
 DB 120 KIREKPLGLFRALDSALTSIFHYDS-----TAAAAFLVILQTTAEASRKYIEGGIIE 174  
 QY 179 IRYN 182  
 DB 175 IPKN 178

## RESULT 12

RIP1\_CUCFI STANDARD; PRT; 286 AA.  
 AC Q9FRX4;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Putative ribosome-inactivating protein precursor (tRNA N-glycosidase)  
 DE (EC 3.2.2.22).  
 OS Cucumis figarei.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.  
 OX NCBI\_TaxID=131071;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Yamada T., Ohki S.T., Osaki T.;  
 RT "Cloning and analysis of a cDNA coding a putative ribosome-  
 RT inactivating protein from Cucumis figarei.";  
 RL Plant Biotechnol. 17:337-340(2000).  
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one  
 CC specific adenosine on the 28S rRNA.  
 CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 CC TYPE 1 RIP SUBFAMILY.

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 CC -----  
 DR EMBL; AB045560; BAB:9677.1; -.  
 DR HSSP; P16094; LAHC.  
 DR InterPro; IPR001574; RIP.  
 DR Pfam; PF00161; RIP; 1.  
 DR PRINTS; PR00396; SHIGARICIN.  
 DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
 KW Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;  
 KW Toxin; Signal.  
 FT SIGNAL 1 21  
 FT CHAIN 22 286  
 FT ACT SITE 185 185  
 FT CARBOHYD 103 103  
 FT CARBOHYD 110 110  
 FT CARBOHYD 252 252  
 FT SEQUENCE 286 AA; 31771 MW; 4EFD4966E604DA41 CRC64;

Query Match 29.8%; Score 283; DB 1; Length 286;  
 Best Local Similarity 33.0%; Pred. No. 2.8e-19;  
 Matches 61; Conservative 45; Mismatches 61; Indels 18; Gaps 4;

QY 9 INFTTAGATVQSYTNFIRAVRGRLTNR---VGLPI-----NQRFILVELSNHAELSVT 58  
 DB 28 VKFSLGSHKYSKFTLSMRNALPNAGDIYINPLVPSISGSRRLVQLSNYEYGTIT 87  
 QY 59 LALDVTNAVYVGRAGNSAYFFHDPNQEDAEATHLFTDQVNRYYTFAFGNDRLQLAG 118  
 DB 88 MAVDVTNVYIMGLVNGTSYFF---NETDAQASKFVFGQTSITLIPYSNGYKQLQSVAR 144  
 QY 119 NLRENIELGNPLEEALISALYYSTGTQTLPTLARSFIIICMISEARFOYIEGMRTR 178  
 DB 145 KERDSIPGLFALDSALTSIYIYDSRSPFI-----AFLVLIQTAAEARKYIEKQIIDR 199  
 QY 179 IRYN 183  
 DB 200 ISVK 204

## RESULT 13

```

RIPA_LUCFY          STANDARD;          PRT;   277 AA.
ID  RIPA_LUCFY
AC  Q00465;
DT  01-DEC-1992 (Rel. 24, Created)
DT  01-DEC-1992 (Rel. 24, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Ribosome-inactivating protein luffin-alpha precursor (rRNA
DE  N-glycosidase) (EC 3.2.2.22).
OS  Luffa cylindrica (Smooth loofah) (Sponge gourd).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC  euroids 1; Cucurbitales; Cucurbitaceae; Luffa.
OX  NCBI_TaxID=3670;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Seed;
RC  MEDLINE=92288316; PubMed=1600156;
RA  Kataoka J., Habuka N., Miyano M., Masuta C., Koiwai A.;
RT  "Nucleotide sequence of cDNA encoding alpha-luffin, a ribosome-
RT  inactivating protein from Luffa cylindrica."
RL  Plant Mol. Biol. 18:1199-1202(1992).
CC  -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC  specific adenosine on the 28S rRNA.
CC  -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC  TYPE 1 RIP SUBFAMILY.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
CC  EMBL; X62371; CAA44229.1; -
CC  PIR; S22494; S22494.
CC  HSSP; P16094; 1AHC.
CC  InterPro; IPR001574; RIP.
CC  Pfam; PF00161; RIP; 1.
CC  PRINTS; PR00396; SHIGARICIN.
CC  PROSITE; PS00275; SHIGA_RICIN; 1.
CC  Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
CC  Toxin; Signal.
CC  SIGNAL 1 19 RIBOSOME-INACTIVATING PROTEIN LUFFIN-
CC  CHAIN 20 277 ALPHA.
CC  ACT SITE 179 179 BY SIMILARITY.
CC  SEQUENCE 277 AA; 30212 MW; EA17FC27998C25AC CRC64;
CC  -----
Query Match 29.0%; Score 276; DB 1; Length 277;
Best Local Similarity 33.3%; Pred. No. 1.2e-18;
Matches 62; Conservative 42; Mismatches 62; Indels 20; Gaps 4;
QY 9 INFTTAGATVQSYTNFIRAVRGLNRVGLPN-----ORFILVELSNHAELSV 57
Db 22 VRFSLGSSSTSYKFIGDLKALPSN-CTVYNTILLSSASCASRYTILMTLSNDGKAI 80
QY 58 TLALDVNTNAYVGVNAGNSAYFFHPDQDAEAI THLFTDVQVNRVTFAGGNYDRLEQLA 117
Db 81 TVADVNTNAYVGVNAGNSAYFFHPDQDAEAI THLFTDVQVNRVTFAGGNYDRLEQLA 137
QY 118 GNLEINELGNGLPEAISAALYVYSGTQLPTLARSFLICQIMISEARFOYIEGEMRT 177
Db 138 GKIREKIPGLFALDSAITLTHFYDS-----TAAAAAFVLVIQTAAEAFKXIEGQIIIE 192
QY 178 RIRYNR 183
Db 193 RISKNQ 198
QY 193 RISKNQ 198
PRT; 254 AA.
RESULT 14
MLA_VISAL
ID  MLA_VISAL

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AC  P81446;
DT  15-DEC-1998 (Rel. 37, Created)
DT  15-DEC-1998 (Rel. 37, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Beta-galactoside specific lectin I A chain (MLA) (ML-I A) (rRNA N-
DE  glycosidase) (EC 3.2.2.22).
OS  Viscum album (European mistletoe).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC  Santalales; Santalaceae; Viscum.
OX  NCBI_TaxID=3972;
RN  [1]
RP  SEQUENCE.
RC  STRAIN=Subsp. album;
RC  MEDLINE=97134581; PubMed=8980141;
RA  Soler M.H., Stoeva S., Schwaborn C., Wilhelm S., Stiefel T.,
RA  Voelter W.;
RT  "Complete amino acid sequence of the A chain of mistletoe lectin I.";
RL  FEBS Lett. 399:153-157(1996).
CC  -1- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN
CC  SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
CC  SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S rRNA. THE
CC  B CHAIN BINDS TO CELL RECEPTORS AND PROBABLY FACILITATES THE ENTRY
CC  INTO THE CELL OF THE A CHAIN; B CHAINS ARE ALSO RESPONSIBLE FOR
CC  CELL AGGLUTINATION (LECTIN ACTIVITY).
CC  -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC  specific adenosine on the 28S rRNA.
CC  -1- SUBUNIT: Disulfide-linked dimer of A and B chains.
CC  -1- PHARMACOLOGICAL: Due to its immunomodulatory effects it is being
CC  studied in clinical trials in cancer patients as it may slow the
CC  growth of cancer cells and be an effective treatment for solid
CC  tumors.
CC  -1- MISCELLANEOUS: TWO ISOFORMS OF MLA EXIST: GLYCOSYLATED FORM MLA
CC  AND NON-GLYCOSYLATED FORM MLA'.
CC  -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC  TYPE 2 RIP SUBFAMILY.
CC  PIR; PD0018; PD0018.
CC  HSSP; P11140; 1ABR.
CC  InterPro; IPR001574; RIP.
CC  Pfam; PF00161; RIP; 1.
CC  PRINTS; PR00396; SHIGARICIN.
CC  PROSITE; PS00275; SHIGA_RICIN; FALSE_NEG.
CC  Plant defense; Hydrolase; Toxin; Repeat; Glycoprotein; Lectin.
CC  ACT SITE 165 165 BY SIMILARITY.
CC  SEQUENCE 254 AA; 28478 MW; 53BAF98D3E0FF67 CRC64;
CC  -----
Query Match 28.7%; Score 272.5; DB 1; Length 254;
Best Local Similarity 37.8%; Pred. No. 2.3e-18;
Matches 79; Conservative 30; Mismatches 53; Indels 47; Gaps 10;
QY 13 TAGATVQSYTNFIRAVR-----GRLTNRVGL-----PIN--ORFILVELSNHAELSVTL 59
Db 9 THQTTGEEYFRFTILLRDYVSSGSFSEIPLLRQSTIPVSDAQRFLVELTNQGDQSVTA 68
QY 60 ALDVNTNAYVGVNAGNSAYFFHPDQDAEAI THLFTDVQVNRVTFAGGNYDRLEQLAGN 119
Db 69 ALDVNTNAYVGVNAGNSAYFFHPDQDAEAI THLFTDVQVNRVTFAGGNYDRLEQLAGN 124

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Query Match      28.4%; Score 270.5; DB 1; Length 286;
Best Local Similarity 35.4%; Pred. No. 4.1e-18;
Matches 64; Conservative 40; Mismatches 58; Indels 19; Gaps 5;

QY 9 INFTTAGATVQSYTNFIRAVKGRLTNR---VGLPI-----NORFIIIVELSNHAEISVT 58
Db 25 VSEFLSGADPRSYGMFIKDLNALPFREKVVNIPLLLPSVSGAGRYLLMHELVYDCKTIT 84
QY 59 LALDVTNAYVVGVRAGNSAYFFHPDNQEDAE-AITHLFTDVQNRKRYTFAFGNVDRLLEQLA 117
Db 85 VAVDVTNVYIMGYLADTTTSYFF--NEPAAELASQYVFRDARRKITLPSYSGNYERLQIAA 141
QY 118 GNLRNIELNGPLEEALSAIYYYSTGGTQPLTLARSLFICIMISEAARFQXIEGEMRT 177
Db 142 GKPREKIPIGLPALDLSAISTLLHYDS-----TAAAGALLVLIQTAAARFKYTEQQIQE 196
QY 178 R 178
Db 197 R 197
```

Search completed: February 10, 2004, 16:23:25  
Job time : 6.17124 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:17:00 ; Search time 24.6849 Seconds  
(without alignments)  
1933.961 Million cell updates/sec

Title: US-10-083-336A-9

Perfect score: 951

Sequence: 1 IFFKQVPIINFTTAGATVQS.....ARFQYIEGEMRTIRYNRRS 185

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23.3\*

1: sp\_archaea.\*

2: sp\_bacteria.\*

3: sp\_fungi.\*

4: sp\_human.\*

5: sp\_invertebrate.\*

6: sp\_mammal.\*

7: sp\_mhc.\*

8: sp\_organelle.\*

9: sp\_phage.\*

10: sp\_plant.\*

11: sp\_rodent.\*

12: sp\_virus.\*

13: sp\_vertebrate.\*

14: sp\_unclassified.\*

15: sp\_rvirus.\*

16: sp\_bacteriaph.\*

17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	934.5	98.3	541	Q41174	ricinus com
2	370	38.9	580	Q41174	ricinus com
3	370	38.9	580	Q41174	ricinus com
4	366	38.5	581	Q41174	ricinus com
5	364	38.3	549	Q41174	ricinus com
6	335.5	35.3	289	Q41174	ricinus com
7	333.5	35.1	289	Q41174	ricinus com
8	327.5	34.4	247	Q41174	ricinus com
9	326	34.3	563	Q41174	ricinus com
10	323	34.0	564	Q41174	ricinus com
11	313.5	33.0	270	Q41174	ricinus com
12	310.5	32.6	270	Q41174	ricinus com
13	310	32.6	252	Q41174	ricinus com
14	308	32.4	528	Q41174	ricinus com
15	306	32.2	563	Q41174	ricinus com
16	306	32.2	563	Q41174	ricinus com

17	303	31.9	547	10	Q9M6E9	Q9M6E9 abrus preca
18	301.5	31.7	565	10	Q04071	Q04071 sambucus ni
19	297	31.2	278	10	Q00980	Q00980 luffa cylin
20	293	30.8	566	10	Q04072	Q04072 sambucus ni
21	291	30.6	252	10	Q38761	Q38761 abrus preca
22	285	30.0	251	10	Q96236	Q96236 abrus preca
23	284	29.9	251	10	Q96237	Q96237 abrus preca
24	278	29.2	251	10	Q96235	Q96235 abrus preca
25	276.5	29.1	249	10	Q8LKQ5	Q8LKQ5 viscum albu
26	270.5	28.4	592	10	Q8W2E7	Q8W2E7 iris hollan
27	269.5	28.3	264	10	Q9FSH2	Q9FSH2 momordica c
28	268.5	28.2	254	10	Q8LKQ6	Q8LKQ6 viscum albu
29	268.5	28.2	570	10	Q41358	Q41358 sambucus ni
30	266.5	28.0	286	10	Q9FUV7	Q9FUV7 momordica c
31	265	27.9	604	10	Q9M654	Q9M654 polyodonat
32	264	27.8	565	10	Q8W243	Q8W243 viscum albu
33	262.5	27.6	570	10	Q22415	Q22415 sambucus ni
34	261.5	27.5	286	10	Q41257	Q41257 momordica c
35	261.5	27.5	531	10	Q8RXH6	Q8RXH6 viscum albu
36	259.5	27.3	249	10	Q8RXH7	Q8RXH7 viscum albu
37	259.5	27.3	573	10	Q8W2E8	Q8W2E8 iris hollan
38	257.5	27.1	251	10	Q8LKQ4	Q8LKQ4 viscum albu
39	256.5	27.0	293	10	Q8S452	Q8S452 jatropa cu
40	253.5	26.7	569	10	P93543	P93543 sambucus ni
41	242.5	25.5	258	10	Q9S9E4	Q9S9E4 gelonium mu
42	241.5	25.4	293	10	Q8VYU0	Q8VYU0 jatropa cu
43	240	25.2	603	10	Q9M653	Q9M653 polyodonat
44	238	25.0	203	10	Q8RY69	Q8RY69 synostemma
45	238	25.0	275	10	Q8HLY4	Q8HLY4 synostemma

## ALIGNMENTS

### RESULT 1

Q41174	Q41174	PRELIMINARY;	PRT;	541 AA.
AC	Q41174;			
DT	01-NOV-1996 (TrEMBLrel. 01, Created)			
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)			
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)			
DB	Proridin A chain (EC 3.2.2.22) (rRNA N-glycosidase)			
DE	(Fragment)			
OS	Ricinus communis (Castor bean)			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eurosidis I; Malpighiales; Euphorbiaceae; Ricinus.			
OX	NCBI_TaxID=9988;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92338377; PubMed=1633311;			
RA	Roberts L.M., Tregear J.W., Lord J.M.;			
RT	"Molecular cloning of ricin."			
RL	Targeted diagn. Ther. 7:81-97(1992).			
CC	!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE			
CC	!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.			
DR	EMBL; S40366; AB22582.1; -			
DR	HSP; P02879; IBER6.			
DR	InterPro; IPR000772; Ricin_B_lectin.			
DR	InterPro; IPR001574; RIP.			
DR	InterPro; IPR001400; Somatotropin.			
DR	Pfam; PF00652; Ricin_B_lectin; 6.			
DR	Pfam; PF00161; RIP; I_lectin; 6.			
DR	PRINTS; PR00396; SHIGARICIN.			
DR	SMART; SM00458; RICIN; 2.			
DR	PROSITE; PS02031; RICIN_B_LCTIN; 2.			
DR	PROSITE; PS02075; SHIGA_RICIN; 1.			
DR	PROSITE; PS00338; SOMATOTROPIN_2; 1.			
KW	Hydrolase; Toxin.			
FT	NON_TER			
SEQUENCE	541 AA; 60281 MW; 2B7B2CDEF1F2E9D9 CRC64;			

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Query Match      98.3%; Score 934.5; DB 10; Length 541;
Best Local Similarity 93.4%; Pred. No. 1.8e-80;
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 IFPKQYPIINFTAGATVQSYTNFIRAVGRGLT-----NRVGLPINQRFILV 47
DB 1 IFPKQYPIINFTAGATVQSYTNFIRAVGRGLTGDVVRHDIPLVLRNKGILPINQRFILV 60

QY 48 ELSNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYRTFAFG 107
DB 61 ELSNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYRTFAFG 120

QY 108 GNYDRLEQAGLNRENELGNGLPLEEALISALYYSTGTQPLTLARSLFIQIMISEAAR 167
DB 121 GNYDRLEQAGLNRENELGNGLPLEEALISALYYSTGTQPLTLARSLFIQIMISEAAR 180

QY 168 FOYIEGEMRTRIRYNRRS 185
DB 181 FOYIEGEMRTRIRYNRRS 198

RESULT 2
Q94BW3 PRELIMINARY; PRT; 580 AA.
AC Q94BW3;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE Type 2 ribosome-inactivating protein cinnamomin III precursor
DE (EC 3.2.2.22) (rRNA N-glycosidase).
OS Cinnamomum camphora (Camphor tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
OX NCBI_TaxID=13429;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang Q., Gong Z.Z., Liu W.Y.;
RT "Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
RT genes encoding cinnamomin proteins and study of their expression
RT patterns."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC EMBL; AY039802; AAK82460.1; -
CC InterPro; IPR000772; Ricin_B_lectin.
CC Pfam; PF00652; Ricin_B_lectin; 6.
CC Pfam; PF00161; RIP; 1.
CC PRINTS; PR00396; SHIGARICIN.
CC SMART; SM00458; RICIN; 2.
CC PROSITE; PS50231; RICIN_B_LECTIN; 2.
KW Hydrolase; Signal; Toxin.
FT SIGNAL 1 32
FT CHAIN 33 580
FT TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT CINNAMOMIN III.
SQ SEQUENCE 580 AA; 64421 MW; 940D10F01E7FB558 CRC64;

Query Match      38.9%; Score 370; DB 10; Length 580;
Best Local Similarity 47.6%; Pred. No. 1.2e-26;
Matches 99; Conservative 26; Mismatches 54; Indels 18; Gaps 5;

QY 6 YPIINFTTAGATVQSYTNFIRAVGRGLTN-----RVGLPINQRFILVELSN-H 52
DB 33 YQTVTFITKNATKTSYTFIEALRAQLASGEHPGIPVMRSTVDSKEFIVELSNWA 92

QY 53 AELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYRTFAFGNYDR 112
DB 93 ADSPVLAVDVNTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYRTFAFGNYDR 149

QY 113 LEQAGLNRENELGNGLPLEEALISALYYSTGTQPLTLARSLFIQIMISEAARFOYIE 172
DB 150 LERVAGERREIEILLGMDPLENAISLWNL--NQORALARSLIVVIQMVAEAVRFRFIE 207

Query Match      38.9%; Score 370; DB 10; Length 580;
Best Local Similarity 47.6%; Pred. No. 1.2e-26;
Matches 99; Conservative 26; Mismatches 54; Indels 18; Gaps 5;

QY 6 YPIINFTTAGATVQSYTNFIRAVGRGLTN-----RVGLPINQRFILVELSN-H 52
DB 33 YQTVTFITKNATKTSYTFIEALRAQLASGEHPGIPVMRSTVDSKEFIVELSNWA 92

QY 53 AELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYRTFAFGNYDR 112
DB 93 ADSPVLAVDVNTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYRTFAFGNYDR 149

QY 113 LEQAGLNRENELGNGLPLEEALISALYYSTGTQPLTLARSLFIQIMISEAARFOYIE 172
DB 150 LERVAGERREIEILLGMDPLENAISLWNL--NQORALARSLIVVIQMVAEAVRFRFIE 207

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QY 173 GEMRTRI 179
DB 208 YRVRESI 214

RESULT 3
Q94BW4 PRELIMINARY; PRT; 580 AA.
AC Q94BW4;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE Type 2 ribosome-inactivating protein cinnamomin II precursor
DE (EC 3.2.2.22) (rRNA N-glycosidase).
OS Cinnamomum camphora (Camphor tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
OX NCBI_TaxID=13429;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang Q., Gong Z.Z., Liu W.Y.;
RT "Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
RT genes encoding cinnamomin proteins and study of their expression
RT patterns."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC EMBL; AY039802; AAK82459.1; -
CC InterPro; IPR000772; Ricin_B_lectin.
CC Pfam; PF00652; Ricin_B_lectin; 6.
CC Pfam; PF00161; RIP; 1.
CC PRINTS; PR00396; SHIGARICIN.
CC SMART; SM00458; RICIN; 2.
CC PROSITE; PS50231; RICIN_B_LECTIN; 2.
KW Hydrolase; Signal; Toxin.
FT SIGNAL 1 32
FT CHAIN 33 580
FT TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT CINNAMOMIN II.
SQ SEQUENCE 580 AA; 64265 MW; 37E4289ECCCECBFF CRC64;

Query Match      38.9%; Score 370; DB 10; Length 580;
Best Local Similarity 47.6%; Pred. No. 1.2e-26;
Matches 89; Conservative 28; Mismatches 52; Indels 18; Gaps 6;

QY 6 YPIINFTTAGATVQSYTNFIRAVGRGLTNRV---GLPI-----NQRFILVELSN-H 52
DB 33 YQTVTFITKNATKTSYTFIEALRAQLASGEHPGIPVMRSTVDSKEFIVELSNWA 92

QY 53 AELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYRTFAFGNYDR 112
DB 93 ADSPVLAVDVNTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYRTFAFGNYDR 149

QY 113 LEQAGLNRENELGNGLPLEEALISALYYSTGTQPLTLARSLFIQIMISEAARFOYIE 172
DB 150 LERVAGERREIEILLGMDPLENAISAL--WTSNLNQORALARSLIVVIQMVAEAVRFRFIE 207

Query Match      38.9%; Score 370; DB 10; Length 580;
Best Local Similarity 47.6%; Pred. No. 1.2e-26;
Matches 89; Conservative 28; Mismatches 52; Indels 18; Gaps 6;

QY 6 YPIINFTTAGATVQSYTNFIRAVGRGLTNRV---GLPI-----NQRFILVELSN-H 52
DB 33 YQTVTFITKNATKTSYTFIEALRAQLASGEHPGIPVMRSTVDSKEFIVELSNWA 92

QY 53 AELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYRTFAFGNYDR 112
DB 93 ADSPVLAVDVNTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYRTFAFGNYDR 149

QY 113 LEQAGLNRENELGNGLPLEEALISALYYSTGTQPLTLARSLFIQIMISEAARFOYIE 172
DB 150 LERVAGERREIEILLGMDPLENAISAL--WTSNLNQORALARSLIVVIQMVAEAVRFRFIE 207

RESULT 4
Q94BW5 PRELIMINARY; PRT; 581 AA.
AC Q94BW5;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE Type 2 ribosome-inactivating protein cinnamomin I precursor
DE (EC 3.2.2.22) (rRNA N-glycosidase).

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DR	InterPro; IPR000772; Ricin_B_lectin.	
DR	InterPro; IPR001574; RIP.	
DR	Pfam; PF00652; Ricin_B_lectin; 5.	
DR	Pfam; PF00161; RIP; 1.	
DR	PRINTS; PR00396; SHIGARICIN.	
DR	SMART; SM00458; RICIN; 2.	
DR	PROSITE; PS00231; RICIN_B_LECTIN; 2.	
KW	Hydrolase; Toxin.	
FT	NON_TER	1
SQ	SEQUENCE	549 AA; 60648 MW; 02607FE607CA44B0 CRC64;
Query Match		
Best Local Similarity		
Matches		
89; Conservative 25; Mismatches 55; Indels 18; Gaps 5		
QY	6 YPIINFETTAGATVQSYTNFIRAVRGLTN-----RVGLPINQRFILVELSN-H	52
DB	1 YQIVTFTTKATKTSYTFQIEALRAQLASGEHPHGVMRERSTVPDSKGRFILVELSNWA	60
QY	53 AELSVTLALDVTNAYVVGYPAGNSAYFFHPDNDQEDAEATHLFTDVQNRITYFAFGNYDR	112
DB	61 ADSFVTLADVTNAYVYVYRTGSGFPLEDRNPDP--PAIENLLPDTK-RYTFPFSGSYTD	117
QY	113 LEQAGNLNREINELGNCPLEEAISALYYSTGGTQLPETLARSEFTICQMISEAAARFOYIE	172
DB	118 LEVGAGERREIILGMDPLENAISALWISNL--NQQRALKSLVIVQMWAEAVRFRFIE	175
QY	173 GEMRTRI 179	
DB	176 YRVGSI 182	
RESULT 6		
Q94KE4	Q94KE4 PRELIMINARY; PRT; 289 AA.	
ID	Q94KE4	
AC	Q94KE4; 2001 (TrEMBLrel. 19, Created)	
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)	
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)	
DE	Trichosanthin precursor (BC 3.2.2.22) (rRNA N-glycosidase).	
GN	TCS.	
OS	Trichosanthes kirilowii (Mongolian snake-gourd).	
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;	
OC	eurosid I; Cucurbitales; Cucurbitaceae; Trichosanthes.	
OX	NCBI_TaxID=3677;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Xuan H., Wang L., Wang Y., An C., Chen Z.;	
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.	
CC	-1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.	
CC	-1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.	
DR	EMBL; AF367252; AAK52960.1; --	
DR	InterPro; IPR001574; RIP.	
DR	Pfam; PF00161; RIP; 1.	
DR	PRINTS; PR00396; SHIGARICIN.	
DR	PROSITE; PS00275; SHIGA RICIN; 1.	
KW	Hydrolase; Signal; Toxin.	
FT	SIGNAL	1 23
FT	CHAIN	24 270
SQ	SEQUENCE	289 AA; 31706 MW; A6D5602549CA5657 CRC64;
Query Match		
Best Local Similarity		
Matches		
71; Conservative 42; Mismatches 50; Indels 19; Gaps 4		
QY	9 INFTTAGATVQSYTNFIRAVRGLTN-----RVGLPINQRFILVELSNHAEISVT	58
DB	25 VSRFLSGATSSSYGVFISNLKALPNERKLYDIPLLRSSLPGSQRYALHILNTYADETIS	84
QY	59 LALDVTNAYVVGYPAGNSAYFFHPDNDQEDA-EATHLFTDVQNRITYFAFGNYDRLEQLA	117

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Db      85 VAIDVTNVMYGRAGDTSYFF---NEASATEAAKYVFKDMRKITLTPSYGNVERLQTAA 141
QY      118 GNLENIELNGPLSEEAISALYVYSTGTQPLTARSFIICQMISEARFYIEGEMRT 177
Db      142 GKIRENIPLGLPALDSAITTLFFYNAN-----SAASALMWLIQSTSEARFYIEQIQGK 196
QY      178 RI 179
Db      197 RV 198

RESULT 7
Q41216 PRELIMINARY; PRT; 289 AA.
AC Q41216; (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Trichosanthin (EC 3.2.2.22) (rRNA N-glycosidase).
GN TRICHOSANTHIN, TCS.
OS Trichosanthin kirilowii (Mongolian snake-gourd).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthin.
OX NCBI_TaxID=3677;

SEQUENCE FROM N.A.
Query Match 35.1%; Score 333.5; DB 10; Length 289;
Best Local Similarity 39.0%; Pred. No. 1.4e-23;
Matches 71; Conservative 42; Mismatches 50; Indels 19; Gaps 4;

QY      9 INFTTAGATVQSYTNFIRAVRGLTN-----RVGLPINQRFLVLSNHAELSVT 58
Db      25 VSFRLSGATSSSYGVFISNLRKALPNRKYLDIPLLRSSLPQSGQRYALVHLTNVADETIS 84
QY      59 LALDVTNAYVVGVRAGNSAYFFHPDQEDA-EAITHLFTDVQNRVYTFAGGNYDRLEQLA 117
Db      85 VAIDVTNVMYGRAGDTSYFF---NEASATEAAKYVFKDMRKITLTPSYGNVERLQTAA 141
QY      118 GNLENIELNGPLSEEAISALYVYSTGTQPLTARSFIICQMISEARFYIEGEMRT 177
Db      142 GKIRENIPLGLPALDSAITTLFFYNAN-----SAASALMWLIQSTSEARFYIEQIQGK 196
QY      178 RI 179
Db      197 RV 198

RESULT 8
Q9LRE3 PRELIMINARY; PRT; 247 AA.
AC Q9LRE3; 2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Trichobakin (EC 3.2.2.22) (rRNA N-glycosidase) (fragment).
GN TBK.

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OS Trichosanthin sp. Bac Kan 8-98.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthin.
OX NCBI_TaxID=118182;

SEQUENCE FROM N.A.
Phan Van Chi, Nguyen Thuy Ha, Le Tran Binh.
RT "Genomic DNA Clone for mature typ-1 ribosome-inactivating protein from
Trichosanthin sp. sample 01 Bac Kan 8-98 Vien CNSH (Hanoi).";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 28S RNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; AB039324; BAA92530.1; -.
DR HSSP; P09989; 1MRJ.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Hydrolase; Toxin.
FT NON TER 1
FT TER 247
SQ SEQUENCE 247 AA; 27199 MW; 89811AC32892F03F CRC64;

Query Match 34.4%; Score 327.5; DB 10; Length 247;
Best Local Similarity 39.0%; Pred. No. 4.2e-23;
Matches 71; Conservative 42; Mismatches 50; Indels 19; Gaps 4;

QY      9 INFTTAGATVQSYTNFIRAVRGLTN-----RVGLPINQRFLVLSNHAELSVT 58
Db      25 VSFRLSGATSSSYGVFISNLRKALPNRKYLDIPLLRSSLPQSGQRYALVHLTNVADETIS 61
QY      59 LALDVTNAYVVGVRAGNSAYFFHPDQEDA-EAITHLFTDVQNRVYTFAGGNYDRLEQLA 117
Db      62 VAIDVTNVMYGRAGDTSYFF---NEASATEAAKYVFKDMRKITLTPSYGNVERLQTAA 118
QY      118 GNLENIELNGPLSEEAISALYVYSTGTQPLTARSFIICQMISEARFYIEGEMRT 177
Db      119 GKIRENIPLGLPALDSAITTLFFYNAN-----SAASALMWLIQSTSEARFYIEQIQGK 173
QY      178 RI 179
Db      174 RV 175

RESULT 9
Q04367 PRELIMINARY; PRT; 563 AA.
AC Q04367; (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Ribosome inactivating protein precursor (EC 3.2.2.22) (rRNA
N-glycosidase).
OS Sambucus nigra (European elder).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.
OX NCBI_TaxID=4202;

SEQUENCE FROM N.A.
RX MEDLINE=98112023; PubMed=9450339;
RA Van Damme E.J., Roy S., Barre A., Rouge P., Van Leuven F.,
Feumans W.J.;
RT "The major elderberry (Sambucus nigra) fruit protein is a lectin
derived from a truncated type 2 ribosome-inactivating protein.";
RL Plant J. 12:1251-1260(1997).
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 28S RNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; U76524; AAC15886.1; -.
DR HSSP; P02879; 2AAI.

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DR InterPro; IPR000772; Ricin\_B\_lectin.

DR InterPro; IPR001574; RIP.

DR Pfam; PF00652; Ricin\_B\_lectin; 6.

DR Pfam; PF00161; RIP; 1.

DR PRINTS; PR00396; SHIGARICIN.

DR SMART; SM00458; RICIN; 2.

DR PROSITE; PS00231; RICIN\_B\_LECTIN; 2.

DR PROSITE; PS00275; SHIGA\_RICIN; 1.

KW Hydrolase; Signal; Toxin.

FT SIGNAL 1 25 POTENTIAL.

FT CHAIN 26 297 RIBOSOME INACTIVATING PROTEIN, A CHAIN.

FT CHAIN 298 563 RIBOSOME INACTIVATING PROTEIN, B CHAIN.

SQ SEQUENCE 563 AA; 62336 MW; 3ED2B6C08E796205 CRC64;

Query Match 34.3%; Score 326; DB 10; Length 563;

Best Local Similarity 40.5%; Pred. No. 1.8e-22;

Matches 77; Conservative 37; Mismatches 48; Indels 28; Gaps 6;

QY 6 YPIINFTAGATVQSYTNFIRAVRGRLTRV-----GLP-----INQRFILVELSNH 52

DB 28 YPSVSNLAGAKSATYRDFLNLRDRVATGYEVNGLPVLRRSEVQVKNRFLVLLTNY 87

QY 53 AELSVTALDVTNAYVGVYAGNSAYFFHEDNODAEAI--TLFTDVQNRVTFAGGNY 110

DB 88 NGNTVTLAVDVTNLYVVAFSANANSYFF-----KDATQKSNLFLVQTR-OHTLPFTGNY 141

QY 111 DRLEQAGNLRENIELGNGPLEPAISALYYSTGGTQPLTARSFFICIMISEAARFQY 170

DB 142 DNLETAAGTRESIELGPSLDGATSLYYDE-----SVARSLLVLIQWSEARFRY 194

QY 171 IEGERMTRIR 180

DB 195 IEQEVRRSLQ 204

RESULT 10

Q9AVR2 PRELIMINARY; PRT; 564 AA.

AC Q9AVR2; 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Ribosome-inactivating protein precursor (EC 3.2.2.22) (rRNA

DE N-glycosidase).

GN EBU1.

OS Sambucus ebulus.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.

OX NCBI\_TaxID=28503;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Leaf;

RA Gibbs T., Iglesias R., Perez Y., Ferreras J.M., Citores L.;

RT "Molecular cloning of ebulin 1";

RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE

CC SPECIFIC ADENOSINE ON THE 28S RNA.

CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

DR EMBL; AJ400822; CAC33178.1; --

DR HSP; P02079; 2A4I

DR InterPro; IPR000772; Ricin\_B\_lectin.

DR InterPro; IPR001574; RIP.

DR Pfam; PF00652; Ricin\_B\_lectin; 6.

DR Pfam; PF00161; RIP; 1.

DR PRINTS; PR00396; SHIGARICIN.

DR SMART; SM00458; RICIN; 2.

DR PROSITE; PS00231; RICIN\_B\_LECTIN; 2.

DR PROSITE; PS00275; SHIGA\_RICIN; 1.

KW Glycosidase; Hydrolase; Signal; Toxin.

FT SIGNAL 1 25 POTENTIAL.

FT CHAIN 26 298 EBU1IN L A-CHAIN.

FT CHAIN 299 564 EBU1IN L B-CHAIN.

SQ SEQUENCE 564 AA; 62694 MW; 8261681A6DB55CB8 CRC64;

Query Match 34.0%; Score 323; DB 10; Length 564;

Best Local Similarity 40.0%; Pred. No. 3.5e-22;

Matches 76; Conservative 38; Mismatches 48; Indels 28; Gaps 7;

QY 6 YPIINFTAGATVQSYTNFIRAVRGRLTRV-----GLP-----INQRFILVELSNH 52

DB 28 YPSVSNLAGAKSATYRDFLNLRDRVATGYEVNGLPVLRRSEVQVKNRFLVLLTNY 87

QY 53 AELSVTALDVTNAYVGVYAGNSAYFFHEDNODAEAI--TLFTDVQNRVTFAGGNY 110

DB 88 NGDTVTSADVTLNLYVAFSANGNSYFF-----KDATQKSNLFLGT-TQHTLSFTGNY 141

QY 111 DRLEQAGNLRENIELGNGPLEPAISALYYSTGGTQPLTARSFFICIMISEAARFQY 170

DB 142 DNLETAAGTRESIELGNPLDGAITSIMY--DGG-----VARSLLVLIQWPEAARFRY 194

QY 171 IEGERMTRIR 180

DB 195 IEQEVRRSLQ 204

RESULT 11

Q8LPV7 PRELIMINARY; PRT; 270 AA.

AC Q8LPV7; 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Trichosanthin precursor (EC 3.2.2.22) (rRNA N-glycosidase)

DE (Fragment).

GN TCS.

OS Trichosanthes kirilowii (Mongolian snake-gourd).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.

OX NCBI\_TaxID=3677;

RN [1]

RP SEQUENCE FROM N.A.

RA Yuan H., Wang L., Wang Y., Liu T., An C., Chen Z.;

RT "Trichosanthes kirilowii trichosanthin precursor (TCS) gene";

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE

CC SPECIFIC ADENOSINE ON THE 28S RNA.

CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

DR EMBL; AY082348; AAM22782.1; --

DR InterPro; IPR001574; RIP.

DR Pfam; PF00161; RIP; 1.

DR PRINTS; PR00396; SHIGARICIN.

DR PROSITE; PS00275; SHIGA\_RICIN; 1.

KW Hydrolase; Signal; Toxin.

FT SIGNAL 1 23 POTENTIAL.

FT CHAIN 24 >270 TRICHOSANTHIN.

FT NON TER 270 270

SQ SEQUENCE 270 AA; 23683 MW; 531713B754F9B769 CRC64;

Query Match 33.0%; Score 313.5; DB 10; Length 270;

Best Local Similarity 37.4%; Pred. No. 1e-21;

Matches 68; Conservative 43; Mismatches 52; Indels 19; Gaps 4;

QY 9 INFTTAGATVQSYTNFIRAVRGRLTN-----RVGLPINCORFVLVELSNHAEISVT 58

DB 25 VSPRLSGATSSSYGVFISLNLRKALPEYKLYDIPILRSSLSGSRVALIYLTVADETIS 84

QY 59 LALDVTNAYVGVYAGNSAYFFHEDNODAEAI--TLFTDVQNRVTFAGGNYDRLEQLA 117

DB 85 VALDVTNAYVGVYAGNSAYFFHEDNODAEAI--TLFTDVQNRVTFAGGNYDRLEQLA 141

QY 118 GNLRNIELGNGPLEPAISALYYSTGGTQPLTARSFFICIMISEAARFQYIEGEMRT 177

DB 142 GKIRENIPGLPDLSDAITTLFYNNAN-----SAASALLVLIQSTAEARFKTEQOIGK 196

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

RA Hung C.-H., Lee M.-C., Lee T.-C., Lin J.-Y.;  
 RT "Primary structure of three distinct isobatrins determined by cDNA  
 RL sequencing: conservation and significance."; J. Mol. Biol. 228:263-267(1993).  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 CC -1- SPECIFIC ADENOSINE ON THE 28S RNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 DR EMBL; M98346; AAA32626.1; -.  
 DR HSSP; P11140; 1ABR.  
 DR InterPro; IPR000772; Ricin\_B\_lectin.  
 DR InterPro; IPR001574; RIP.  
 DR Pfam; PF00652; Ricin\_B\_lectin; 6.  
 DR Pfam; PF00161; RIP; 1.  
 DR PRINTS; PR00396; SHIGARICIN.  
 DR SMART; SM00458; RICIN; 2.  
 DR PROSITE; PS00231; RICIN\_B\_LLECTIN; 2.  
 DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
 DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
 KW Hydrolyase; Toxin.  
 FT NON TER 1  
 FT NON TER 528  
 SQ SEQUENCE 528 AA; 58870 MW; 62ED42FB8FFE60F8 CRC64;  
 Query Match 32.4%; Score 308; DB 10; Length 528;  
 Best Local Similarity 42.2%; Pred. No. 8.7e-21;  
 Matches 79; Conservative 23; Mismatches 67; Indels 18; Gaps 5;  
 QY 5 QYPIINFTTAGATVQSYTNFIRAVRGRLTNRV---GLPI-----NORFILVELSNHA 53  
 DB 1 QDQVIKFTTEGATQSQYKQFIEALRQLTGLHIDPVLDPDPTVEERNRYITVELSNSE 60  
 QY 54 ELSVTALDVTNAYVVGVRAGNSAYFFHPDNQEDAEAI--THLFTDVQNRVYFAFGGNYDEL 113  
 DB 61 RESIEGIDVTNAYVYVYRAGSQSYEL---RDAPASASTYLPFGTC-RYSLRFDGSGYGD 116  
 QY 114 EQLAGNLRNIEIENGPLEEATISALYYSTGTQPLTLARSFIIQMISEAAARFOYIEG 173  
 DB 117 ERWAHOTREISLGLQALTHAIS---FLRSGASNDEEKARTLIVLIQMASEAAARVCI 173  
 QY 174 EMEIRIR 180  
 DB 174 RVGSIR 180  
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 Q945S2 PRELIMINARY; PRT; 563 AA.  
 ID Q945S2  
 AC Q945S2  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Ribosome-inactivating protein (EC 3.2.2.22) (rRNA  
 DE N-glycosidase).  
 GN AVL.  
 OS Sambucus nigra (European elder).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.  
 OX NCBI\_TaxID=4202;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Leaf;  
 RA Van Damme E.J.M.;  
 RT "Characterization and cloning of lectins and ribosome-inactivating  
 RL proteins from Sambucus nigra leaves."; SubMITTED (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 CC -1- SPECIFIC ADENOSINE ON THE 28S RNA.  
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.  
 DR EMBL; AF409135; AAL04123.1; -.  
 DR InterPro; IPR000772; Ricin\_B\_lectin.  
 DR InterPro; IPR001574; RIP.  
 DR Pfam; PF00652; Ricin\_B\_lectin; 6.  
 DR Pfam; PF00161; RIP; 1.

DR PRINTS; PR00396; SHIGARICIN.  
 DR SMART; SM00458; RICIN; 2.  
 DR PROSITE; PS00231; RICIN\_B\_LLECTIN; 2.  
 DR PROSITE; PS00275; SHIGA\_RICIN; 1.  
 KW Hydrolyase; Toxin.  
 SQ SEQUENCE 563 AA; 62242 MW; 07F7CBEDCF33BF10 CRC64;  
 Query Match 32.2%; Score 306; DB 10; Length 563;  
 Best Local Similarity 38.4%; Pred. No. 1.5e-20;  
 Matches 73; Conservative 36; Mismatches 53; Indels 28; Gaps 6;  
 QY 6 YPIINFTTAGATVQSYTNFIRAVRGRLTNRV---GLP-----INORFILVELSNH 52  
 DB 28 YPSVFNLDGAKSATYRDFLSNLRKTWATGYEYVNGLPVLRRESEVQVKSRLFVPLTNY 87  
 QY 53 AELSVTALDVTNAYVVGVRAGNSAYFFHPDNQEDAEAI--THLFTDVQNRVYFAFGGNY 110  
 DB 88 NGNTVTTLAVDVTNLYVYVAFSGNANSYFF-----KDQTEVQKSNLFVGTQKQ-TLSFTGNY 141  
 QY 111 DRLEQLAGNLRNIEIENGPLEEATISALYYSTGTQPLTLARSFIIQMISEAAARFOY 170  
 DB 142 DNLETAANTRRRESIELGSPDLGATISLYHGD-----SVARSLLVVIQMVSEAAARFY 194  
 QY 171 IEQEMRTRIR 180  
 DB 195 IEQEVRSIQ 204  
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:13:20 ; Search time 34.0993 Seconds  
(without alignments)  
930.966 Million cell updates/sec

Title: US-10-083-336A-10

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Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*  
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1024	99.5	267	14	Ricin A chain. Un
2	1024	99.5	267	16	Ricin A-chain (RTA
3	1024	99.5	290	18	Ricin A-chain ribo
4	1024	99.5	290	18	Ricin A-chain RIP.
5	1024	99.5	332	8	Ricin A. Escheric
6	1024	99.5	332	8	Sequence of Ricinu
7	1024	99.5	332	10	Ricin A encoded by
8	1024	99.5	554	16	Anti-catact immu
9	1024	99.5	562	10	Ricin D. Ricinus

10	1024	99.5	565	22	AAW78304	Modified castor be
11	1024	99.5	576	8	AAW70326	Sequence of Ricinu
12	1024	99.5	576	18	AAW25787	Castorbean ricin.
13	1024	99.5	576	20	AAW55892	Castor bean ricin
14	1024	99.5	576	21	AAW78592	Ricinus communis r
15	1024	99.5	576	21	AAW78301	Castor bean prepro
16	1024	99.5	576	22	AAW78302	Castor bean prepro
17	1022	99.3	268	14	AAW39570	Sequence of ricin-
18	1021	99.2	565	6	AAW50166	Sequence of prepro
19	1021	99.2	565	22	AAW78300	Castor bean prepro
20	1019	99.0	534	14	AAW39571	Sequence of G-FIT.
21	1017	98.8	574	8	AAW70325	Sequence of Ricinu
22	1016	98.7	200	9	AAW80164	Biosynthetic multi
23	1016	98.7	565	7	AAW60240	Preproricin. Ricin
24	1015	98.6	574	10	AAW94793	DNA sequence of ri
25	1014	98.5	267	13	AAW30722	Ricin A from PIC11
26	1014	98.5	267	21	AAW19265	Amino acid sequenc
27	1013	98.4	332	11	AAW06554	Ricin A gene produ
28	997	96.9	267	16	AAW74176	Ricin A chain (RTA
29	991	96.3	267	14	AAW32430	Ricin A. Syntheti
30	934.5	90.8	540	18	AAW25143	Castor oil plant a
31	934.5	90.8	540	18	AAW21706	Ricin agglutinin A
32	800.5	77.8	534	8	AAW70324	Sequence of Ricin
33	782	76.0	280	10	AAW95648	Trichosanthin anti
34	342	33.2	247	16	AAW67359	Amino acid sequenc
35	342	33.2	247	21	AAW69048	Synthetic alpha-tr
36	342	33.2	248	11	AAW07518	Mature alpha-Trich
37	342	33.2	248	13	AAW25573	Trichosanthin (a r
38	342	33.2	267	18	AAW25140	Trichosanthin. Tr
39	342	33.2	267	18	AAW21703	Trichosanthin from
40	342	33.2	289	11	AAW07514	Trichosanthin from
41	342	33.2	289	13	AAW25572	Trichosanthin prot
42	342	33.2	289	13	AAW25272	Trichosanthin prot
43	342	33.2	289	14	AAW32986	Encodes chinese cu
44	342	33.2	289	15	AAW55129	Alpha-trichosanthi
45	342	33.2	289	18	AAW10468	Chinese cucumber a

#### ALIGNMENTS

RESULT 1  
AAR37290  
ID AAR37290 standard; protein; 267 AA.  
XX AAR37290;  
AC AAR37290;  
XX  
XX 25-MAR-2003 (updated)  
DT 09-JAN-2003 (updated)  
DT 13-SEP-1993 (first entry)  
XX  
XX Ricin A chain.  
DE  
XX  
XX Type II ribosome-inactivating protein; type II RIP; gelonin;  
KW momordin; immunoconjugate; autoimmune disease; cell killing; toxin.  
XX Unidentified.  
OS  
XX  
XX W09309130-A1.  
PN  
XX  
XX 13-MAY-1993.  
PD  
XX  
XX 04-NOV-1992; 92WO-US09487.  
PF  
XX  
XX 04-NOV-1991; 91US-0787567.  
PR  
XX 19-JUN-1992; 92US-0901707.  
XX (XOMA ) XOMA CORP.  
PA  
XX Berhard SL, Better MD, Carroll SF, Lane JA, Lei SP;  
PI WPI; 1993-167617/20.  
XX  
XX

PT Analogues of type I ribosome inactivating protein - useful as  
PT cytotoxic agents, immuno toxins for treating auto immune diseases,  
PT cancer, graft versus host disease and selective cell killing in-vivo  
XX  
XX  
PS Claim 1; Page 92; 163pp; English.  
XX  
XX The invention covers analogues of Type I RIPs. Ricin is a Type II  
CC RIP whose A chain is homologous to plant type I RIPs. The analogues  
CC of the invention have a cysteine available for intermolecular  
CC disulphide bonding at an amino acid position corresp. to a position  
CC not naturally available for bonding; the cys residue is located in  
CC the C-terminal region of the analogue between a position corresp. to  
CC amino acid 251 and the C-terminus of ricin A chain. The analogues are  
CC pref. joined via a disulphide linkage to a molecule which specifically  
CC binds to a target cell, e.g. an antibody fragment.  
CC (Updated on 09-JAN-2003 to add missing OS field.)  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
XX  
SQ Sequence 267 AA;  
Query Match 99.5%; Score 1024; DB 14; Length 267;  
Best Local Similarity 100.0%; Pred. No. 7.5e-101;  
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINORFILV 61  
DB 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINORFILV 60  
QY 62 ELSNHAELSVTALDVTNAYVVGVRAGNSAYFFHPDQEDAEAI THLFTDVQNRYYTFAFG 121  
DB 61 ELSNHAELSVTALDVTNAYVVGVRAGNSAYFFHPDQEDAEAI THLFTDVQNRYYTFAFG 120  
QY 122 GNYDRLEQLAGNLRENIELNGPLPEEAISALYYSTGGTQLPTLARSFIIQIMISEAAR 181  
DB 121 GNYDRLEQLAGNLRENIELNGPLPEEAISALYYSTGGTQLPTLARSFIIQIMISEAAR 180  
QY 182 FOYIEGEMRTRIRYNRNSA 200  
DB 181 FOYIEGEMRTRIRYNRNSA 199

RESULT 2  
AAR63902  
ID AAR63902 standard; protein; 267 AA.  
XX  
XX AC AAR63902;  
XX  
XX 25-MAR-2003 (updated)  
XX 27-JUL-1995 (first entry)  
XX  
XX Ricin A-chain (RTA).  
XX Ricin A chain; RTA; ribosome-inactivating proteins; RIPs;  
XX cytotoxic therapeutic agents; autoimmune disease; cancer;  
XX graft-versus-host disease.  
XX Ricinus communis.  
XX WO9426910-A1.  
XX  
XX 24-NOV-1994.  
XX  
XX 12-MAY-1994; 94WO-US05348.  
XX  
XX 12-MAY-1993; 93US-0064691.  
XX  
XX (XOMA ) XOMA CORP.  
XX  
XX Better MD, Carroll SS, Studnicka GM, Carroll SF;  
XX WPI; 1995-006804/01.  
XX  
XX Polynucleotide(s) encoding type I ribosome-inactivating proteins

PT - which are suitable for use as components of cytotoxic  
PT therapeutic agents.  
XX  
XX Example 3; Fig 1; 221pp; English.  
XX  
XX AAR63902 is the ricin A chain gene product, it is analogous to the  
CC ribosome-inactivating proteins (RIPs) described in AAR63903-R63911.  
CC RIPs are the key components of cytotoxic therapeutic agents (CTAs),  
CC which include gene fusion products and immunoconjugates. CTAs may  
CC be used to selectively eliminate any cell type to which a RIP  
CC component is targeted, by the specific binding capacity of the  
CC second component of the agent. They can be used in the treatment  
CC of diseases where the elimination of a particular cell type is  
CC desired, such as autoimmune disease, cancer and graft-versus-host  
CC disease.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
XX  
SQ Sequence 267 AA;  
Query Match 99.5%; Score 1024; DB 16; Length 267;  
Best Local Similarity 100.0%; Pred. No. 7.5e-101;  
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINORFILV 61  
DB 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINORFILV 60  
QY 62 ELSNHAELSVTALDVTNAYVVGVRAGNSAYFFHPDQEDAEAI THLFTDVQNRYYTFAFG 121  
DB 61 ELSNHAELSVTALDVTNAYVVGVRAGNSAYFFHPDQEDAEAI THLFTDVQNRYYTFAFG 120  
QY 122 GNYDRLEQLAGNLRENIELNGPLPEEAISALYYSTGGTQLPTLARSFIIQIMISEAAR 181  
DB 121 GNYDRLEQLAGNLRENIELNGPLPEEAISALYYSTGGTQLPTLARSFIIQIMISEAAR 180  
QY 182 FOYIEGEMRTRIRYNRNSA 200  
DB 181 FOYIEGEMRTRIRYNRNSA 199

RESULT 3  
AAR63902  
ID AAR63902 standard; Protein; 290 AA.  
XX  
XX AC AAR63902;  
XX  
XX 25-MAR-2003 (updated)  
XX 02-DEC-1997 (first entry)  
XX  
XX Ricin A-chain ribosome inhibitory protein inactive precursor.  
XX  
XX Maize; proRIP; ribosome inactivating protein; alpha; beta subunit;  
XX internal linker; Barley Translation Inhibitor; Trichosanthin;  
XX Ricin A-chain; Abrin-A chain; Saporin; SLT-1; Luffin A; MAP;  
XX Ricinus communis agglutinin; Momordin; PAP-S; Luffin-B; Dianthin 30;  
XX therapeutic toxin; tumour cell targeted; protein synthesis inhibitor;  
XX post-translational modification; cancer; neoplasia; HIV; AIDS;  
XX human immunodeficiency virus; acquired immune deficiency syndrome.  
XX  
XX Synthetic.  
XX  
XX US5646026-A.  
XX  
XX 08-JUL-1997.  
XX  
XX 07-JUN-1995; 95US-0485286.  
XX  
XX 09-DEC-1992; 92US-0987927.  
XX 11-JUN-1990; 90US-0535636.  
XX 26-JAN-1995; 95US-0378761.  
XX 07-JUN-1995; 95US-0485286.  
XX  
XX (DOWC ) DOWELANCO.  
XX

XX Hey TD, Morgan AER, Walsh TA;  
 XX WPI; 1997-362934/33.  
 XX DNA encoding pro-ribosome inactivating proteins - inactive  
 PT precursors of ribosome inactivating proteins; can be expressed in  
 PT eukaryotic cells without causing cell death  
 XX  
 PS Claim 4; Column 91-94; 186pp; English.  
 XX  
 CC AAW25136 represents a Ricin A-chain ribosome inhibitory protein (RIP)  
 CC which was engineered to contain a selectively removable internal peptide  
 CC linker sequence separating the alpha and beta units of the RIP. When  
 CC separated the two units regain activity and are capable of inactivating  
 CC eukaryotic ribosomes and hence preventing protein production. Many  
 CC different RIPs may be produced with an internal linker including  
 CC maize RIP, Trichosanthin, Ricin A-chain, Abrin-A A-chain and  
 CC Saporin. The RIPs can be used in the construction of therapeutic  
 CC toxins targeted to specific cells such as tumour cells via the  
 CC attachment of a targeting polypeptide, e.g. a monoclonal antibody.  
 CC A further use is in HIV therapy (see US4869903). There is interest  
 CC in expressing RIP recombinantly in host eukaryotic cells, because of  
 CC the capacity to provide correct post-translational processing. However,  
 CC RIPs effectively inhibit protein synthesis in eukaryotic cells resulting  
 CC in cell death. Since the inactive RIP proteins are not cytotoxic to  
 CC eukaryotic cells, they can be recombinantly expressed in such cells and  
 CC then converted to active RIP proteins.  
 CC (Updated on 25-MAR-2003 to correct PF field.)  
 XX  
 SQ Sequence 290 AA;  
 Query Match 99.5%; Score 1024; DB 18; Length 290;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-101;  
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 IFPKQYPIINFATTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNVRVGLPINQRFILV 61  
 DB 25 IFPKQYPIINFATTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNVRVGLPINQRFILV 84  
 QY 62 ELSNHAELSVTLLADVNTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAPG 121  
 DB 85 ELSNHAELSVTLLADVNTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAPG 144  
 QY 122 GNYDRLEQLAGNLRENIELNGPLLEEAISALYYSTGTQLTPLARSFFICQMISEAAR 181  
 DB 145 GNYDRLEQLAGNLRENIELNGPLLEEAISALYYSTGTQLTPLARSFFICQMISEAAR 204  
 QY 182 FOYIEGEMTRIRYNRRA 200  
 DB 205 FOYIEGEMTRIRYNRRA 223  
 RESULT 4  
 AAW21699  
 ID AAW21699 standard; Protein; 290 AA.  
 XX  
 AC AAW21699; .  
 XX  
 XX 25-MAR-2003 (updated)  
 DT 26-SEP-1997 (first entry)  
 XX  
 DE Ricin A-chain RIP.  
 XX  
 KW pro-Ribosome Inactivating Protein; proRIP; peptide linker; cancer;  
 KW inactivation; eukaryotic ribosome; alpha fragment; beta fragment;  
 KW inhibitor; protein synthesis; N-glycosidase; glycosidic bond; liver;  
 KW rat; ribosomal 28S RNA; cellular proliferation; HIV-infected T cell.  
 XX  
 OS Ricinus communis.  
 XX  
 XX Key Location/Qualifiers  
 FH 152..162  
 FT

FT  
 FT  
 XX  
 PN US5635384-A.  
 XX  
 PD 03-JUN-1997.  
 XX  
 PF 26-JAN-1995; 95US-0378761.  
 PR 09-DEC-1992; 92US-0987927.  
 PR 11-JUN-1990; 90US-0535636.  
 PR 26-JAN-1995; 95US-0378761.  
 XX (DOWC ) DOWELANCO.  
 PA Hey TD, Morgan AER, Walsh TA;  
 PI WPI; 1997-309831/28.  
 XX  
 DR Inactive precursor of maize ribosome-inactivating protein - also  
 XX chimeric ribosome-inactivating protein precursors containing  
 PT internal linker sequences  
 XX  
 PS Claim 2; Column 91-94; 121pp; English.  
 XX  
 CC The sequences given in AAW21698-710 represent Ribosome Inactivating  
 CC Proteins (RIP's), which may be used in the construction of the  
 CC proRIP of the invention. The proRIP has a selectively removable,  
 CC internal peptide linker. The precursor sequence is incapable of  
 CC inactivating eukaryotic ribosomes, but can be converted by removal  
 CC of the linker into a protein having alpha and beta fragments and being  
 CC capable of inactivating eukaryotic ribosomes. RIPs are potent  
 CC inhibitors of eukaryotic protein synthesis. They possess a highly  
 CC specific N-glycosidase activity which cleaves the glycosidic bond of  
 CC adenine 4324 of rat liver ribosomal 28S RNA. RIP's selectively inhibit  
 CC cellular proliferation of cells, e.g. cancer cells and HIV-infected T  
 CC cells. The inactive proRIP proteins make it possible to provide protein  
 CC synthesis inhibitors with uses in practical and improved ways not before  
 CC possible. The RIP can be used to make cytotoxic conjugates.  
 CC (Updated on 25-MAR-2003 to correct PF field.)  
 XX  
 SQ Sequence 290 AA;  
 Query Match 99.5%; Score 1024; DB 18; Length 290;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-101;  
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 IFPKQYPIINFATTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNVRVGLPINQRFILV 61  
 DB 25 IFPKQYPIINFATTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNVRVGLPINQRFILV 84  
 QY 62 ELSNHAELSVTLLADVNTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAPG 121  
 DB 85 ELSNHAELSVTLLADVNTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAPG 144  
 QY 122 GNYDRLEQLAGNLRENIELNGPLLEEAISALYYSTGTQLTPLARSFFICQMISEAAR 181  
 DB 145 GNYDRLEQLAGNLRENIELNGPLLEEAISALYYSTGTQLTPLARSFFICQMISEAAR 204  
 QY 182 FOYIEGEMTRIRYNRRA 200  
 DB 205 FOYIEGEMTRIRYNRRA 223  
 RESULT 5  
 AAW20097  
 ID AAW20097 standard; protein; 332 AA.  
 XX  
 AC AAW20097;  
 XX  
 XX 09-APR-1991 (first entry)  
 DT  
 DE Ricin A.

/note= "Position of possible insertion of internal  
 peptide linker sequence"



XX Ricin A; Met-aminopeptidase.  
 XX Escherichia coli.  
 XX EP219237-A.  
 XX 22-APR-1987.  
 XX 19-SEP-1986; 86EP-0307242.  
 XX 06-MAY-1986; 86US-0860330.  
 XX 20-SEP-1985; 85US-0778414.  
 XX (CETU ) CETUS CORP.  
 XX Benbassat A, Bauer KA, Chang S, Chang SY;  
 XX WPI; 1987-110172/16.  
 XX N-PSDB; AAN70152.  
 XX N-terminal methionine free proteins prodn. - by using host  
 XX transformed with vector to express a methionine-amino-peptidase  
 XX Disclosure; Fig. 4; 20pp; English.  
 XX Ricin A may be produced in a form which lacks an N-terminal Met  
 XX using Met-aminopeptidase from E.coli.  
 XX Sequence 332 AA;

Query Match 99.5%; Score 1024; DB 8; Length 332;  
 Best Local Similarity 100.0%; Pred. No. 1e-100;  
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 IFPKQYPIINFITTAGATVQSYTNFIRAVRGLTTGADVVRHEIPVLPNRVGLPINORFILV 61  
 DB 36 IFPKQYPIINFITTAGATVQSYTNFIRAVRGLTTGADVVRHEIPVLPNRVGLPINORFILV 95  
 QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAG 121  
 DB 96 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAG 155  
 QY 122 GNYDRLEQLAGNLRENIELGNGLPEEASALYYSTGTQPLTLARSFIIQIMISEAR 181  
 DB 156 GNYDRLEQLAGNLRENIELGNGLPEEASALYYSTGTQPLTLARSFIIQIMISEAR 215  
 QY 182 FOYIEGEMTRIRYNR 200  
 DB 216 FOYIEGEMTRIRYNR 234

RESULT 6  
 AAP70838  
 ID AAP70838 standard; protein; 332 AA.  
 XX AAP70838;  
 XX 25-MAR-2003 (updated)  
 DT 18-FEB-1991 (first entry)  
 XX Sequence of Ricinus communis castor beans ricin toxin (RT or ricin)  
 DE A protein encoded by pR123.  
 XX Lectin; toxin protein; cytotoxic; cytostatic; castor bean;  
 KW plant toxin.  
 XX Ricinus communis.  
 XX Key Location/Qualifiers  
 FH Region 1..32  
 FT /notes="Leader"  
 FT Region 33..302

FT Region /note="A-chain"  
 FT 315..332  
 XX /note="B-chain"  
 XX EP237676-A.  
 XX 23-SEP-1987.  
 XX 13-NOV-1986; 86EP-0308877.  
 XX 07-MAR-1986; 86US-0837583.  
 XX (CETU ) CETUS CORP.  
 XX (CHIR ) CHIRON CORP.  
 XX Piatak M;  
 XX WPI; 1987-265177/38.  
 XX N-PSDB; AAN70519.

New non-glycosylated ricin precursor and toxin etc. - are prepd.  
 by recombinant DNA procedures with specific isolation steps for  
 purer and soluble prods.

Disclosure; Fig 1; 112pp; English.

The full-length sequences encoding ricin A (AAN70520), ricin D  
 (AAN70525), putative ricin E (AAN70526) and RCA (AAN70524) in precursor  
 form were obt'd. using messenger RNA to obtain a cDNA library, and  
 then probing the library to retrieve the desired cDNA inserts. The  
 library was probed using the 35-mer given in AAN70514. Figure 4 (see  
 AAN70520, AAN70521, AAN70522) shows the nucleotide sequences of three  
 plasmids contg. cDNA inserts obt'd. by probing a cDNA library for  
 sequences encoding ricin B using the probe in AAN70517. The cDNA  
 inserts can be placed into expression vectors. Site-directed  
 mutagenesis may be used to place an ATG start codon and a HindIII  
 site at the beginning of the mature protein (see AAN70518). The  
 coding sequences of the inserts can be ligated into expression  
 vectors contg. the PhdA promoter-operator and leader sequence  
 (AAN70523) and suitable retroregulators.  
 CC (Updated on 25-MAR-2003 to correct PA field.)

Sequence 332 AA;

Query Match 99.5%; Score 1024; DB 8; Length 332;  
 Best Local Similarity 100.0%; Pred. No. 1e-100;  
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFPKQYPIINFITTAGATVQSYTNFIRAVRGLTTGADVVRHEIPVLPNRVGLPINORFILV 61  
 DB 36 IFPKQYPIINFITTAGATVQSYTNFIRAVRGLTTGADVVRHEIPVLPNRVGLPINORFILV 95  
 QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAG 121  
 DB 96 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAG 155  
 QY 122 GNYDRLEQLAGNLRENIELGNGLPEEASALYYSTGTQPLTLARSFIIQIMISEAR 181  
 DB 156 GNYDRLEQLAGNLRENIELGNGLPEEASALYYSTGTQPLTLARSFIIQIMISEAR 215  
 QY 182 FOYIEGEMTRIRYNR 200  
 DB 216 FOYIEGEMTRIRYNR 234

RESULT 7  
 AAP95639  
 ID AAP95639 standard; protein; 332 AA.  
 XX AAP95639;  
 XX 25-MAR-2003 (updated)  
 DT 31-OCT-2002 (updated)

DT XX 13-AUG-1990 (first entry)  
 DE XX Ricin A encoded by insert from plasmid pRA123.  
 XX Plasmid pRA123; ricin-A; ricin-B; cytotoxicity.  
 KW Ricinus communis.  
 OS Synthetic.  
 XX Key Location/Qualifiers  
 FH 1..35  
 FT Peptide /label= leader sequence  
 FT Peptide 36..302  
 FT Peptide /label=A-chain  
 FT Peptide 303..314  
 FT Peptide /label=linker  
 FT Peptide 315..332  
 FT Peptide /label=B-chain  
 XX EP335476-A.  
 PN XX  
 XX 04-OCT-1989.  
 PD 19-JAN-1989; 89EP-0201162.  
 PF 08-FEB-1984; 84US-0578115.  
 PR 08-FEB-1984; 84US-0578121.  
 PR 09-FEB-1984; 84US-0578122.  
 PR 07-SEP-1984; 84US-0648759.  
 PR 20-SEP-1984; 84US-0653515.  
 XX (CETU ) CETUS CORPORATION.  
 PA Gelfand D, Lawyer FC, Horn G, Greenfield L, Nitecki D, Kaplan D;  
 PI Piatak MJ;  
 XX WPI; 1989-286959/40.  
 DR N-PSDB; AAN91281.  
 XX Recombinant vectors expressing ricin chains or diphtheria toxin -used for  
 PT prodn. of new immunotoxin conjugates with monoclonal antibodies, having  
 PT high cell specificity and good extracellular stability.  
 XX Disclosure; Fig 14; 54pp; English.  
 XX Plasmid RA123 (ATCC No. 39799) carries the entire coding sequence for  
 CC ricin A, as well as codons for 12 AAs joining the A to the B chain.  
 CC Following modification for ease of manipulation the plasmid was used to  
 CC construct expression vectors which express the conjugates in  
 CC host cells.  
 CC (Updated on 31-OCT-2002 to add missing OS field.)  
 CC (Updated on 25-MAR-2003 to correct PF field.)  
 CC (Updated on 25-MAR-2003 to correct PR field.)  
 CC (Updated on 25-MAR-2003 to correct PI field.)  
 XX Sequence 332 AA;  
 SQ Query Match 99.5%; Score 1024; DB 10; Length 332;  
 Best Local Similarity 100.0%; Pred. No. 1e-100;  
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 IFPKQYDIIINFTAGATVQSYTNFIRAVRGRLTTGADVREHIVLPNVRGIPINOREILY 61  
 DB 36 IFPKQYDIIINFTAGATVQSYTNFIRAVRGRLTTGADVREHIVLPNVRGIPINOREILY 95  
 QY 62 ELSNHAELSVTLADVTNAYVVGVRAGNSAYFFHPDQDEAEATHTLFTDVQNRYYTFAFG 121  
 DB 96 ELSNHAELSVTLADVTNAYVVGVRAGNSAYFFHPDQDEAEATHTLFTDVQNRYYTFAFG 155  
 QY 122 GNYDRLEQLAGNLENIELGNGLPEEAISALYYSTGQTQLPTLARSFIICQMISPAAR 181  
 DB 156 GNYDRLEQLAGNLENIELGNGLPEEAISALYYSTGQTQLPTLARSFIICQMISPAAR 215

QY 182 FQYIEGEMRTRIRYNRRA 200  
 DB 216 FQYIEGEMRTRIRYNRRA 234  
 RESULT 8  
 AAR70827  
 ID AAR70827 standard; Protein; 554 AA.  
 XX  
 AC AAR70827;  
 XX 25-MAR-2003 (updated)  
 DT 31-AUG-1995 (first entry)  
 XX Anti-cataract immunotoxin.  
 DE Immunotoxin; heavy chain; light chain; variable region; antibody;  
 KW ricin-A; cytostatic; cataract; lens opacification; epithelial cell;  
 KW PHB19; 4197X; monoclonal antibody; Mab.  
 XX Synthetic.  
 OS Key Location/Qualifiers  
 FH 1..27  
 FT Peptide /label= Sig\_peptide  
 FT /note= "phoA signal sequence"  
 FT Domain 28..145  
 FT /label= HEAVY  
 FT /note= "Mab 4197X heavy chain"  
 FT Peptide 148..166  
 FT /label= LINKER  
 FT Domain 169..274  
 FT /label= LIGHT  
 FT /note= "Mab 419X light chain"  
 FT Domain 276..544  
 FT /label= RICIN-A  
 FT Peptide 549..554  
 FT /label= TAG  
 FT /note= "hexa-histidine tail"  
 XX WO9503828-A1.  
 PN 09-FEB-1995.  
 PD 15-JUL-1994; 94WO-US07919.  
 XX 02-AUG-1993; 93US-0101329.  
 PR (HOUS-) HOUSTON BIOTECHNOLOGY INC.  
 XX Gould RM, Kelleher PJ, Wallace TL, Wood MS;  
 PI WPI; 1995-082036/11.  
 DR N-PSDB; AAQ85386.  
 XX New single chain immuno:toxin - binds specifically to epithelial  
 PT cells, for inhibiting development of sec. cataracts after  
 PT extra:capular cataract extraction.  
 XX Disclosure; Fig.4; 68pp; English.  
 CC The immunotoxin given in AAR70827 comprises the heavy and light chain  
 CC variable regions of anti-lens epithelium I9G3 Mab 4197X linked to  
 CC ricin-A and a hexa-histidine tag. The DNA construct encoding the  
 CC immunotoxin was expressed from PHB19 in E. coli.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX Sequence 554 AA;  
 SQ Query Match 99.5%; Score 1024; DB 16; Length 554;  
 Best Local Similarity 100.0%; Pred. No. 2e-100;  
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHIEPVLNVRGLPINQRFILV 61  
 DB 278 IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHIEPVLNVRGLPINQRFILV 337  
 QY 62 ELSNHAELSVTLADVTNAYVVGVRAGNSAYFFPHDPNQEDAEATHLFTDVQNRYYTFAFG 121  
 DB 338 ELSNHAELSVTLADVTNAYVVGVRAGNSAYFFPHDPNQEDAEATHLFTDVQNRYYTFAFG 397  
 QY 122 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFFIICIMISEAAR 181  
 DB 398 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFFIICIMISEAAR 457  
 QY 182 FOYIEGEMTRIRYNRRSA 200  
 DB 458 FOYIEGEMTRIRYNRRSA 476  
 RESULT 9  
 AAP90079  
 ID AAP90079 standard; protein; 562 AA.  
 AC AAP90079;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 01-NOV-1989 (first entry)  
 XX  
 DE Ricin D.  
 XX  
 KW Ricin D; Ricinus communis; castor beans; Zanicariensis variety;  
 KW modified; lectin binding removed; reduced cell binding  
 XX  
 OS Ricinus communis (castor beans).  
 XX  
 PN WO8904839-A.  
 XX  
 PD 01-JUN-1989.  
 XX  
 PF 23-NOV-1988; 88WO-US04238.  
 XX  
 PR 24-NOV-1987; 87US-0124735.  
 XX  
 PA (GEMY ) GENETICS INST INC.  
 XX  
 PI Brown EL, Jones S;  
 XX  
 DR WPI; 1989-178366/24.  
 DR N-PSDB; AAN90068.  
 XX  
 PT Modified ricin molecules and toxin conjugates  
 PT - in which the lectin binding function of the B chain  
 PT is removed or diminished to reduce cell binding.  
 XX  
 PS Disclosure; fig 1; Sipp; English.  
 XX  
 CC Ricin D (see corresp. AAN90068) found on the EcoRI-HindIII fragment  
 CC of DNA from Ricinus communis, Zanicariensis variety. Patent  
 CC discloses many modifications of ricin in which the lectin binding  
 CC function of the B chain is diminished or removed, and conjugation  
 CC to toxins to eliminate cell binding.  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 CC (Updated on 25-MAR-2003 to correct PI field.)  
 XX  
 SQ Sequence 562 AA;  
 Query Match 99.5%; Score 1024; DB 10; Length 562;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-100;  
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHIEPVLNVRGLPINQRFILV 61  
 DB 36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHIEPVLNVRGLPINQRFILV 95  
 QY 62 ELSNHAELSVTLADVTNAYVVGVRAGNSAYFFPHDPNQEDAEATHLFTDVQNRYYTFAFG 121

DB 96 ELSNHAELSVTLADVTNAYVVGVRAGNSAYFFPHDPNQEDAEATHLFTDVQNRYYTFAFG 155  
 QY 122 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFFIICIMISEAAR 181  
 DB 156 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFFIICIMISEAAR 215  
 QY 182 FOYIEGEMTRIRYNRRSA 200  
 DB 216 FOYIEGEMTRIRYNRRSA 234  
 RESULT 10  
 AAG78304  
 ID AAG78304 standard; Protein; 565 AA.  
 XX  
 AC AAG78304;  
 XX  
 DT 27-NOV-2001 (first entry)  
 XX  
 DE Modified castor bean preprorizin (SEQ ID 10).  
 KW Castor bean plant; preprorizin; ricin; A chain; B chain;  
 KW human immunodeficiency virus infection; HIV; toxin; antiviral agent;  
 KW retroviral infection; anti-HIV; virucide; viral protease.  
 XX  
 OS Chimeric - Ricinus communis  
 OS Chimeric - Human immunodeficiency virus type 2.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..24  
 FT Protein /label= Signal\_peptide  
 FT 25..565  
 FT /label= Prorizin  
 FT /note= "Prorizin consists of the ricin A chain, a linker  
 FT peptide, and the ricin B chain. Prorizin is  
 FT proteolytically cleaved between the A chain and  
 FT the linker to yield mature ricin"  
 FT Protein 25..291  
 FT /label= Ricin\_A\_chain  
 FT /note= "N-glycosidase"  
 FT 292..303  
 FT /label= Linker\_peptide  
 FT Cleavage-site 296..297  
 FT /label= HIV\_protease\_cleavage\_site  
 FT Protein 304..565  
 FT /label= Ricin\_B\_chain  
 FT /note= "Galactose/N-acetylglactosamine-binding lectin"  
 XX  
 PN WO200160393-A1.  
 XX  
 PD 23-AUG-2001.  
 XX  
 PF 15-FEB-2001; 2001WO-US05282.  
 XX  
 PR 16-FEB-2000; 2000US-0182759.  
 XX  
 PA (BECH-) BECHTEL BWXT IDAHO LLC.  
 XX  
 PI Keener WK, Ward TE;  
 XX  
 DR WPI; 2001-581908/65.  
 DR N-PSDB; AAI64145.  
 XX  
 PT Novel composition comprising toxin e.g., ricin based antiviral compound  
 PT useful for treating viral infections such as human immunodeficiency  
 PT virus infection.  
 XX  
 PS Example 1; Page 59-63; 66pp; English.  
 XX  
 CC The sequence relates to the amino acid sequence of a modified preprorizin  
 CC protein encoded by AAI64145. The invention relates to a novel toxin  
 CC (e.g. ricin) based antiviral agent which is toxic to virus-infected

CC cells, but non-toxic to uninfected cells. The invention has anti-HIV and  
 CC virucide activities. The agent is able to enter all HIV susceptible  
 CC cells, and not just cells known to act as host cells for the virus. The  
 CC antiviral agent remains inert in a cell unless the cell is infected  
 CC with the HIV virus, where the viral protease activates it. Ricin's  
 CC mechanism of action is through inactivation of cellular ribosomes and  
 CC enhancement of binding of the antiviral agent to galactose residues on  
 CC cell surfaces, and its cellular internalisation. The invention is useful  
 CC for treating human immunodeficiency virus infection and other viral  
 CC infections, especially retroviral infections. The antiviral agent is  
 CC activated in viral particles or early-stage infected cells, killing the  
 CC cells upon infection and effectively preventing the integration of the  
 CC viral genome into the host genome thereby preventing the latency/rebound  
 CC problem.  
 XX  
 XX Sequence 565 AA;

Query Match 99.5%; Score 1024; DB 22; Length 565;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-100;  
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 IFPKQYPIINFATTAGATVQSYTNFIRAVRGLTTGADVREHPEIPVLPNRVGLPINQRFILV 61  
 Db 25 IFPKQYPIINFATTAGATVQSYTNFIRAVRGLTTGADVREHPEIPVLPNRVGLPINQRFILV 84  
 QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEAIHTLFTDVQNRVTFAPG 121  
 Db 85 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEAIHTLFTDVQNRVTFAPG 144  
 QY 122 GNYDRLEQLAGNLRENIELNGPLLEAISALYYSTGGTQPLTLARSFICIQMISEAAR 181  
 Db 145 GNYDRLEQLAGNLRENIELNGPLLEAISALYYSTGGTQPLTLARSFICIQMISEAAR 204  
 QY 182 FOYIEGEMTRIRYNRSA 200  
 Db 205 FOYIEGEMTRIRYNRSA 223

RESULT 11  
 AAP70326  
 ID AAP70326 standard; Protein; 576 AA.

XX AAP70326;  
 AC AAP70326;  
 XX 25-MAR-2003 (updated)  
 DT 21-MAY-1991 (first entry)  
 XX Sequence of Ricinus communis (castor bean) Ricin toxin  
 DE (RT or ricin) B precursor encoded by pRT38.  
 XX Lectin; toxin protein; cytotoxic; cytostatic; castor bean;  
 KW plant toxin.  
 XX Ricinus communis.

XX Key Location/Qualifiers  
 FH Region 1..35 /note= "leader"  
 FT Region 36..302 /note= "A-chain"  
 FT Region 315..576 /note= "B-chain"  
 FT

XX EP237676-A.  
 PN  
 XX 23-SEP-1987.  
 PD  
 XX 13-NOV-1986; 86EP-0308877.  
 XX  
 XX 07-MAR-1986; 86US-0837583.  
 PR  
 XX (CETU ) CETUS CORP.  
 PA (CHIR ) CHIRON CORP.  
 PA

XX Piatlak M;  
 PI  
 XX WPI; 1987-265177/38.  
 DR N-PSDB; AAN70526.

XX New non-glycosylated ricin precursor and toxin etc. - are prepd.  
 PT by recombinant DNA procedures with specific isolation steps for  
 FT purer and soluble products.  
 XX  
 PS Disclosure; Fig 14(1-2); 112pp; English.

XX The full length sequences encoding ricin A (AAN70520), ricin D  
 CC (AAN70525) putative ricin E (AAN70526) and RCA (AAN70524) in precursor  
 CC form were obtained, using the messenger RNA to obtain a cDNA library, and  
 CC then probing the library to retrieve the desired cDNA inserts. The  
 CC library was probed using the 35-mer given in AAN70514. Figure 4 (see  
 CC AAN70520, AAN70521, AAN70522), shows the nucleotide sequences of three  
 CC plasmids containing cDNA inserts obtained by probing a cDNA library  
 CC for sequences encoding ricin B using the probe in AAN70517. The cDNA  
 CC inserts can be placed into expression vectors. Site-directed  
 CC mutagenesis may be used to place an ATG start codon and a HindIII  
 CC site at the beginning of the mature protein, (see AAN70518). The  
 CC coding sequences of the inserts can be ligated into expression  
 CC vectors containing the phoA promoter-operator and leader sequence  
 CC (AAN70523) and suitable retroregulators.  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX

Sequence 576 AA;

Query Match 99.5%; Score 1024; DB 8; Length 576;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-100;  
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFPKQYPIINFATTAGATVQSYTNFIRAVRGLTTGADVREHPEIPVLPNRVGLPINQRFILV 61  
 Db 36 IFPKQYPIINFATTAGATVQSYTNFIRAVRGLTTGADVREHPEIPVLPNRVGLPINQRFILV 95  
 QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEAIHTLFTDVQNRVTFAPG 121  
 Db 96 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEAIHTLFTDVQNRVTFAPG 155  
 QY 122 GNYDRLEQLAGNLRENIELNGPLLEAISALYYSTGGTQPLTLARSFICIQMISEAAR 181  
 Db 156 GNYDRLEQLAGNLRENIELNGPLLEAISALYYSTGGTQPLTLARSFICIQMISEAAR 215  
 QY 182 FOYIEGEMTRIRYNRSA 200  
 Db 216 FOYIEGEMTRIRYNRSA 234

RESULT 12  
 AAW25787  
 ID AAW25787 standard; Protein; 576 AA.

XX AAW25787;  
 AC AAW25787;  
 XX 25-MAR-2003 (updated)  
 DT 27-MAR-1998 (first entry)  
 XX Castorbean ricin.

XX Ricin; cytotoxin; hybrid protein; cell delivery;  
 KW cell binding ligand; translocation domain; diphtheria toxin B';  
 KW interleukin-2; T-cell lymphoma; organ rejection; therapy.

XX Ricinus communis.  
 XX Key Location/Qualifiers  
 FH Peptide 1..35 /label= Sig\_peptide  
 FT Protein 36..302 /label= A-domain  
 FT

```

FT Peptide 303..314
FT /label= Linker
FT Domain 315..576
FT /label= B-domain
XX
XX US5668255-A.
XX
XX 16-SEP-1997.
XX
XX 04-AUG-1993; 93US-0102387.
XX
XX 27-JUN-1991; 91US-0722484.
XX 07-JUN-1984; 84US-0618199.
XX 25-APR-1985; 85US-0726808.
XX 07-JUN-1985; 85US-0742554.
XX 22-DEC-1989; 89US-0456095.
XX 14-JUN-1990; 90US-0538276.
XX 04-AUG-1993; 93US-0102387.
XX (SERA-) SERAGEN INC.
XX
XX Murphy JR;
XX
XX WPI; 1997-470103/43.
XX N-PSDB; AAT91638.
XX
XX New hybrid molecules for delivery of agents to cells - comprise a
XX binding domain of a cell binding ligand and a portion of a
XX translocation domain of a protein
XX
XX Example 4; Fig 11A-B; 30pp; English.
XX
XX This polypeptide comprises the castorbean cytotoxin, ricin.
XX DNA (see AAT91638) encoding the enzymatic A domain and a portion
XX of the A-to-B linker peptide of ricin was used to construct a
XX ricin-diphtheria toxin B'-interleukin-2 gene that was expressed in
XX E. coli. The hybrid protein can be isolated and used to treat
XX conditions involving over-production of cells bearing IL2 receptors,
XX such as certain T-cell lymphomas and organ transplant rejection
XX crises. The hybrid inactivates ribosomes in cells bearing IL2
XX receptors, resulting in cessation of protein synthesis and death of
XX target cells. Claimed hybrid proteins comprise a translocation
XX domain and a cell binding domain from e.g. a hormone, growth factor
XX or polypeptide toxin. The hybrid molecules can be used for the
XX delivery of agents (e.g. therapeutic genes, toxins, detectable
XX labels) into cells. The use of a translocation mechanism ensures
XX that the hybrid will be effective in relatively low doses, since a
XX high proportion of the substance of interest will be taken into the
XX targeted cells. The hybrid molecules can be manufactured as a
XX single hybrid recombinant protein, permitting reproducibility,
XX consistency, and the precise control of composition.
XX (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Query Match 99.5%; Score 1024; DB 18; Length 576;
XX Best Local Similarity 100.0%; Pred. No. 2.1e-100;
XX Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 2 IFPKQYPIINFNTAGATVQSYTNFIRAVRGLTTGADVREHPVLPNVRVGLPINQRFILV 61
XX
Db 36 IFPKQYPIINFNTAGATVQSYTNFIRAVRGLTTGADVREHPVLPNVRVGLPINQRFILV 95
XX
QY 62 ELSNHAELSVTLALDVTNAYVGVYRAGNSAYFFHPDNQEDAEAIHTLFTDVQNRVTFAPG 121
XX
Db 96 ELSNHAELSVTLALDVTNAYVGVYRAGNSAYFFHPDNQEDAEAIHTLFTDVQNRVTFAPG 155
XX
QY 122 GNYDRLEQLAGNLRNIELNGNPLBEAISALYYVSTGGTQLPTLARSFFIICQMISEAAR 181
XX
Db 156 GNYDRLEQLAGNLRNIELNGNPLBEAISALYYVSTGGTQLPTLARSFFIICQMISEAAR 215
XX
QY 182 FOYIEGEMTRIRYNRRA 200
XX

```

```

Db 216 FOYIEGEMTRIRYNRRA 234
XX
XX RESULT 13
XX AAY55892
XX ID AAY55892 standard; Protein; 576 AA.
XX
XX AC AAY55892;
XX
XX 15-FEB-2000 (first entry)
XX
XX Castor bean ricin toxin.
XX
XX Recombinant; hybrid; binding domain; ligand; animal cell; diphtheria;
XX translocation domain; botulinum; neurotoxin; ricin; cholera; tetanus;
XX shiga-like toxin; pertussis; translocation; cytoplasmic membrane; HIV;
XX cytosol; therapy; genetic deficiency disease; enzyme; co-factor; poison;
XX adipocyte; cancer; virus; infection; antibody.
XX
XX Ricinus communis.
XX
XX US5965406-A.
XX
XX 12-OCT-1999.
XX
XX 07-JUN-1995; 95US-0488246.
XX
XX 04-AUG-1993; 93US-0102387.
XX 07-JUN-1984; 84US-0618199.
XX 27-JUN-1991; 91US-0722484.
XX 25-APR-1985; 85US-0726808.
XX 07-JUN-1985; 85US-0742554.
XX 22-DEC-1989; 89US-0456095.
XX 14-JUN-1990; 90US-0538276.
XX (SERA-) SERAGEN INC.
XX
XX Murphy JR;
XX
XX WPI; 1999-632431/54.
XX N-PSDB; AAZ30663.
XX
XX Recombinant DNA molecule encoding a three part hybrid protein used in
XX the treatment of Aids and genetic deficiency diseases -
XX
XX Example 4; Fig 11; 3lpp; English.
XX
XX The invention relates to a recombinant DNA molecule encoding a hybrid
XX protein comprising three parts: (a) the first part comprises a portion
XX of the binding domain of a cell-binding polypeptide ligand allowing the
XX hybrid protein to bind to an animal cell; (b) the second part comprises
XX a portion of a translocation domain of a naturally occurring protein
XX selected from diphtheria toxin, botulinum neurotoxin, ricin, cholera
XX toxin, LT toxin, C3 toxin, shiga-like toxin, pertussis toxin and tetanus
XX toxin, which translocate the third part of the across the cytoplasmic
XX membrane into the cytosol of the cell; and (c) the third part comprises
XX a polypeptide entity to be introduced into the cell, which is non-native
XX to the naturally occurring protein of (b). This sequence represents the
XX Castor bean ricin toxin sequence for use in generating the hybrid of the
XX invention. The hybrid molecule enables the direction of appropriate
XX therapy to affected cells, allowing them to function properly and
XX alleviate or cure the disease. The hybrid is especially used in treating
XX genetic deficiency diseases, by delivering to affected cells an enzyme
XX supplying the missing function, to supplementing cellular levels of a
XX particular enzyme or a scarce precursor or cofactor, to directing toxins
XX or other poisons to destroy particular cells (such as adipocytes, cancer
XX cell, or virus infected-cells), to counteracting viral infections such as
XX HIV, by introducing appropriate antibodies to viral proteins. It is also
XX involved in the process of getting non-therapeutic substances such as
XX detectable labels into cells.
XX
XX Sequence 576 AA;

```

Query Match 99.5%; Score 1024; DB 20; Length 576;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-100;  
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPFKQYPIINFAGATVQSYTNFIRAVRGRLLTGADVRHEIPVLPNRYGLPINQRFILV 61  
 DB 36 IPFKQYPIINFAGATVQSYTNFIRAVRGRLLTGADVRHEIPVLPNRYGLPINQRFILV 95

QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDABAIHTLFTDVQNRVYTFAG 121  
 DB 96 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDABAIHTLFTDVQNRVYTFAG 155

QY 122 GNYDRLEQAGNLRENIELGNGPLERALSALYYSTGGTQPLTARSFICQMISEAAR 181  
 DB 156 GNYDRLEQAGNLRENIELGNGPLERALSALYYSTGGTQPLTARSFICQMISEAAR 215

QY 182 FOYIEGEMTRIRYNNRSA 200  
 DB 216 FOYIEGEMTRIRYNNRSA 234

RESULT 14  
 AAY78592  
 ID AAY78592 standard; Protein; 576 AA.  
 AC AAY78592;  
 XX  
 XX 05-MAY-2000 (first entry)  
 XX  
 XX Ricinus communis ricin protein sequence.  
 XX  
 KW Ricin; toxin; hybrid protein; translocation domain; cell destruction;  
 KW cell binding domain; genetic deficiency disease; cell targeting; cancer;  
 KW adipocyte; enzyme delivery; anti-viral; HIV.  
 XX  
 XX Ricinus communis.  
 OS  
 XX US6022950-A.  
 PN  
 XX 08-FEB-2000.  
 PD  
 XX 07-JUN-1995; 95US-0479510.  
 PF  
 XX 07-JUN-1984; 84US-0618199.  
 PR 27-JUN-1991; 91US-0722484.  
 PR 25-APR-1985; 85US-0726808.  
 PR 07-JUN-1985; 85US-0742554.  
 PR 22-DEC-1989; 89US-0456095.  
 PR 14-JUN-1990; 90US-0538276.  
 PR 04-AUG-1993; 93US-0102387.  
 XX  
 XX (SERA-) SERAGEN INC.  
 PA  
 XX Murphy JR;  
 FI  
 XX WPI: 2000-160390/14.  
 DR N-PSDB; AAZ90019.  
 DR  
 XX New two-part hybrid protein comprising a translocation domain and a  
 PT cell-binding domain, for treating genetic deficiency diseases, cancer  
 PT and HIV infections -  
 PT  
 XX Example 4; Fig 11; 32pp; English.  
 PS  
 XX This sequence represents the Ricinus communis ricin protein sequence. The  
 CC toxin can be included in the hybrid protein of the invention and used to  
 CC destroy or modify the cell that the hybrid protein is targeted to. The  
 CC hybrid protein comprises a first part which is a portion of the binding  
 CC domain of a cell-binding ligand, effective to cause the hybrid molecule  
 CC to bind to a cell of an animal. The second part comprises a portion of a  
 CC translocation domain of a naturally occurring protein (e.g. the  
 CC translocation domain of diphtheria toxin) the second part translocates  
 CC the third part across the cytoplasmic membrane and into the cytosol of

CC the cell. The third part comprises a chemical entity to be introduced  
 CC into the cell, where each of the first and third part is non-native with  
 CC respect to naturally occurring protein, and the covalent bond attaching  
 CC the second and third part is cleavable. The toxin represented by the  
 CC present sequence can form part of the third portion of the hybrid  
 CC protein. The cell binding domain binds to a specific cell and the  
 CC translocation domain transfers the hybrid molecule across the cell  
 CC membrane into the cytosol. The third part of the protein, linked to the  
 CC translocation domain through a cleavable bond, can then carry out its  
 CC function. The hybrid molecules are useful for treating genetic deficiency  
 CC diseases by delivering to affected cells an enzyme supplying the missing  
 CC function, to supplement cellular levels of a particular enzyme or a  
 CC scarce precursor or cofactor, to direct toxins or other poisons to  
 CC destroy particular cells (such as adipocytes, cancer cells, or  
 CC virus-infected cells), and to counteract viral infections such as HIV by  
 CC introducing into appropriate cells antibodies to viral proteins.  
 XX  
 SQ Sequence 576 AA;

Query Match 99.5%; Score 1024; DB 21; Length 576;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-100;  
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPFKQYPIINFAGATVQSYTNFIRAVRGRLLTGADVRHEIPVLPNRYGLPINQRFILV 61  
 DB 36 IPFKQYPIINFAGATVQSYTNFIRAVRGRLLTGADVRHEIPVLPNRYGLPINQRFILV 95

QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDABAIHTLFTDVQNRVYTFAG 121  
 DB 96 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDABAIHTLFTDVQNRVYTFAG 155

QY 122 GNYDRLEQAGNLRENIELGNGPLERALSALYYSTGGTQPLTARSFICQMISEAAR 181  
 DB 156 GNYDRLEQAGNLRENIELGNGPLERALSALYYSTGGTQPLTARSFICQMISEAAR 215

QY 182 FOYIEGEMTRIRYNNRSA 200  
 DB 216 FOYIEGEMTRIRYNNRSA 234

RESULT 15  
 AAG78301  
 ID AAG78301 standard; Protein; 576 AA.  
 XX  
 AC AAG78301;  
 XX  
 XX 15-NOV-2001 (first entry)  
 DT  
 XX Castor bean preproricin protein (SEQ ID 2).  
 DE  
 XX Castor bean plant; preproricin; ricin; A chain; B chain;  
 KW human immunodeficiency virus infection; HIV; toxin; antiviral agent;  
 KW retroviral infection; anti-HIV; virucide activity; viral protease.  
 XX  
 OS Ricinus communis.  
 XX  
 XX Location/Qualifiers  
 PH Key  
 FT Peptide 1..35  
 FT /label= Signal peptide  
 FT Protein 36..302  
 FT /label= Ricin A chain  
 FT /note= "N-glycosidase"  
 FT Peptide 303..314  
 FT /label= Linker peptide  
 FT /note= "Cleaved during activation of ricin"  
 FT Protein 315..576  
 FT /label= Ricin B chain  
 FT /note= "Galactose/N-acetylgalactosamine-binding lectin"  
 XX  
 XX WO200160393-A1.  
 XX  
 PD 23-AUG-2001.  
 XX

PF 15-FEB-2001; 2001WO-US05282.  
XX  
XX  
PR 16-FEB-2000; 2000US-0182759.  
XX  
XX  
PA (BECH-) BECHTEL BWXT IDAHO LLC.  
XX  
PI Keener WK, Ward TE;  
XX  
XX  
DR WPI; 2001-581908/65.  
XX  
DR N-PSDB; AAI64138.  
XX  
XX  
PT Novel composition comprising toxin e.g., ricin based antiviral compound  
PT useful for treating viral infections such as human immunodeficiency  
PT virus infection.  
XX  
XX  
PS Disclosure; Page 50-54; 66pp; English.  
XX  
XX  
CC The sequence relates to preproricin protein encoded by the DNA sequence  
CC given in AAI64138. The invention relates to a novel toxin (e.g., ricin)  
CC based antiviral agent which is toxic to virus-infected cells, but  
CC non-toxic to uninfected cells. The invention has anti-HIV and virucide  
CC activities. Its mechanism of action is through inactivation of cellular  
CC ribosomes and enhancement of binding of the antiviral agent to galactose  
CC residues on cell surfaces, and its cellular internalisation. The  
CC invention is useful for treating human immunodeficiency virus infection  
CC and other viral infections, especially retroviral infections. The  
CC antiviral agent is activated in viral particles or early-stage infected  
CC cells, killing the cells upon infection and effectively preventing the  
CC integration of the viral genome into the host genome thereby preventing  
CC the latency/rebound problem. The agent enters all HIV susceptible cells,  
CC and not just cells known to act as host cells for the virus. The  
CC antiviral agent remains inert in a cell until degraded in it, unless the  
CC cell is infected with the virus, where the viral protease activates it.  
XX  
XX  
SQ Sequence 576 AA;  
  
Query Match 99.5%; Score 1024; DB 22; Length 576;  
Best Local Similarity 100.0%; Pred. No. 2.le-100;  
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 IFFKQYPIINFATTAGATVQSYTNFIRAVRGRLTTGADVVRHEIPVLPNRVGLPINQRFILV 61  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
36 IFFKQYPIINFATTAGATVQSYTNFIRAVRGRLTTGADVVRHEIPVLPNRVGLPINQRFILV 95  
QY 62 ELSNHAELSVTIALDVTNAYVGVYRAGNSAYFFHPDNOEDAEATHLETDVQNRYYTFAFG 121  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
96 ELSNHAELSVTIALDVTNAYVGVYRAGNSAYFFHPDNOEDAEATHLETDVQNRYYTFAFG 155  
QY 122 GNYDRLEQLAGNLRNIELGNGLPEEATISALYYSTGGTQPLTLARSFTICQMISEAAR 181  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
156 GNYDRLEQLAGNLRNIELGNGLPEEATISALYYSTGGTQPLTLARSFTICQMISEAAR 215  
QY 182 FOYIEGEMRTRIRYNRSA 200  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
216 FOYIEGEMRTRIRYNRSA 234

Search completed: February 10, 2004, 16:22:29  
Job time : 35.0993 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:18:30 ; Search time 11.5641 Seconds  
(without alignments)  
731.761 Million cell updates/sec

Title: US-10-083-336A-10  
Perfect score: 1029  
Sequence: 1 MIFPKQYPIINFTTAGATVQ.....RFQYIEGEMRTIRYNRRSA 200

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/iaa/5A COMB.pap:\*  
2: /cgn2\_6/prodata/1/iaa/5B COMB.pap:\*  
3: /cgn2\_6/prodata/1/iaa/6A COMB.pap:\*  
4: /cgn2\_6/prodata/1/iaa/6B COMB.pap:\*  
5: /cgn2\_6/prodata/1/iaa/PCTUS COMB.pap:\*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1029	100.0	268	2	US-08-356-786-8
2	1029	100.0	534	2	US-08-356-786-10
3	1024	99.5	267	1	US-07-901-707-1
4	1024	99.5	267	1	US-07-988-430-1
5	1024	99.5	267	1	US-08-425-336-1
6	1024	99.5	267	1	US-08-488-113B-1
7	1024	99.5	267	1	US-08-477-484B-1
8	1024	99.5	267	2	US-08-646-360-1
9	1024	99.5	267	3	US-08-839-765-1
10	1024	99.5	267	3	US-09-136-389-1
11	1024	99.5	267	4	US-09-610-838-1
12	1024	99.5	267	5	PCT-US92-09487-1
13	1024	99.5	230	1	US-08-378-761A-27
14	1024	99.5	290	1	US-08-485-286-27
15	1024	99.5	290	6	5248606-4
16	1014	98.5	267	1	US-08-218-303-16
17	1014	98.5	267	2	US-08-338-793D-61
18	1014	98.5	267	4	US-09-538-873-1
19	934.5	90.8	540	1	US-08-378-761A-77
20	934.5	90.8	540	1	US-08-485-286-77
21	342	33.2	247	1	US-08-488-113B-6
22	342	33.2	247	1	US-08-477-484B-6
23	342	33.2	247	2	US-08-646-360-6
24	342	33.2	247	3	US-08-839-765-6
25	342	33.2	247	3	US-09-136-389-6
26	342	33.2	247	4	US-09-610-838-6
27	342	33.2	267	1	US-08-378-761A-74

28	342	33.2	267	1	US-08-485-286-74	Sequence 74, Appl
29	342	33.2	289	1	US-07-923-692C-4	Sequence 4, Appl
30	342	33.2	289	1	US-08-184-237-4	Sequence 4, Appl
31	342	33.2	289	2	US-08-482-920-4	Sequence 4, Appl
32	342	33.2	289	3	US-08-484-341-4	Sequence 4, Appl
33	342	33.2	289	3	US-08-483-502-4	Sequence 4, Appl
34	342	33.2	289	4	US-09-726-651A-4	Sequence 4, Appl
35	341.5	33.2	282	1	US-08-324-301-15	Sequence 15, Appl
36	329.5	32.0	250	1	US-08-378-761A-71	Sequence 71, Appl
37	329.5	32.0	250	1	US-08-485-286-71	Sequence 71, Appl
38	323.5	31.4	251	4	US-09-538-873-3	Sequence 3, Appl
39	312.5	30.4	255	1	US-07-901-707-6	Sequence 6, Appl
40	312.5	30.4	255	1	US-07-988-430-6	Sequence 6, Appl
41	312.5	30.4	255	5	PCT-US92-09487-6	Sequence 6, Appl
42	312.5	30.4	255	5	PCT-US92-09487-6	Sequence 6, Appl
43	312	30.3	248	3	US-08-902-486-7	Sequence 7, Appl
44	312	30.3	290	1	US-08-245-754A-2	Sequence 2, Appl
45	312	30.3	290	2	US-08-597-731-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1  
US-08-356-786-8  
; Sequence 8, Application US/08356786  
; Patent No. 5877305

GENERAL INFORMATION:  
APPLICANT: Huston, James S.  
APPLICANT: Oppermann, Hermann  
APPLICANT: Houston, L. L.  
APPLICANT: Ring, David B.  
TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer  
TITLE OF INVENTION: Marker  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Edmund R. Pitcher, Testa, Hurwitz, & Thibault  
STREET: Exchange Place, 53 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/356,786  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/831,967  
FILING DATE: 06-FEB-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Pitcher, Edmund R.  
REGISTRATION NUMBER: 27,829  
REFERENCE/DOCKET NUMBER: CRP-053  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 268 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-356-786-8

Query Match 100.0%; Score 1029; DB 2; Length 268;  
Best Local Similarity 100.0%; Pred. No. 2.2e-112;  
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRRHEIPVLPNRVGLPINQRFIL 60  
DB 1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRRHEIPVLPNRVGLPINQRFIL 60  
QY 61 VELSNHAEISVTLALDVTNAYVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRYYTFAF 120  
DB 61 VELSNHAEISVTLALDVTNAYVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRYYTFAF 120  
QY 121 GGNVDRLEQLAGNLENIELGNGLPLEEASALYYSTGGTQPLTLARSFFIICQMISEAA 180  
DB 121 GGNVDRLEQLAGNLENIELGNGLPLEEASALYYSTGGTQPLTLARSFFIICQMISEAA 180  
QY 181 RFQYIEGEMTRIRYNRRA 200  
DB 181 RFQYIEGEMTRIRYNRRA 200

## RESULT 2

US-08-356-786-10  
; Sequence 10, Application US/08356786  
; Patent No. 5877305  
; GENERAL INFORMATION:  
; APPLICANT: Huston, James S.  
; APPLICANT: Oppermann, Hermann  
; APPLICANT: Houston, L. L.  
; APPLICANT: Ring, David B.  
; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer  
; TITLE OF INVENTION: Marker  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault  
; STREET: Exchange Place, 53 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/356,786  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/831,967  
; FILING DATE: 06-FEB-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pitcher, Edmund R.  
; REGISTRATION NUMBER: 27,829  
; REFERENCE/DOCKET NUMBER: CRP-053  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 248-7000  
; TELEFAX: (617) 248-7100  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 534 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-356-786-10

Query Match 100.0%; Score 1029; DB 2; Length 534;  
Best Local Similarity 100.0%; Pred. No. 6.1e-112;  
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRRHEIPVLPNRVGLPINQRFIL 60  
DB 3 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRRHEIPVLPNRVGLPINQRFIL 62  
QY 61 VELSNHAEISVTLALDVTNAYVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRYYTFAF 120

DB 63 VELSNHAEISVTLALDVTNAYVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRYYTFAF 122  
QY 121 GGNVDRLEQLAGNLENIELGNGLPLEEASALYYSTGGTQPLTLARSFFIICQMISEAA 180  
DB 123 GGNVDRLEQLAGNLENIELGNGLPLEEASALYYSTGGTQPLTLARSFFIICQMISEAA 182  
QY 181 RFQYIEGEMTRIRYNRRA 200  
DB 183 RFQYIEGEMTRIRYNRRA 202

## RESULT 3

US-07-901-707-1  
; Sequence 1, Application US/07901707  
; Patent No. 5376546  
; GENERAL INFORMATION:  
; APPLICANT: Bernhard, Susan L.  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Steve F.  
; APPLICANT: Lane, Julie A.  
; TITLE OF INVENTION: Materials Comprising and Methods of  
; TITLE OF INVENTION: Composition and Use for Ribosome-Inactivating Proteins  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; STREET: Two First National Plaza, 20 South Clark  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/901,707  
; FILING DATE: 19920619  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5376546 and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27129/30910  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 346-5750  
; TELEFAX: (312) 984-5750  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 267 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-901-707-1

Query Match 99.5%; Score 1024; DB 1; Length 267;  
Best Local Similarity 100.0%; Pred. No. 8.3e-112;  
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRRHEIPVLPNRVGLPINQRFILV 61  
DB 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRRHEIPVLPNRVGLPINQRFILV 60  
QY 62 ELSNHAEISVTLALDVTNAYVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRYYTFAF 121  
DB 61 ELSNHAEISVTLALDVTNAYVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRYYTFAF 120  
QY 122 GGNVDRLEQLAGNLENIELGNGLPLEEASALYYSTGGTQPLTLARSFFIICQMISEAA 181

Db 121 GNYDRLEQAGNLENIELGNGLPLEEALISALYYSTGTQTLPTLARSFICQMISEAAR 180  
QY 182 FOYIEGEMRTRIRYNRSA 200  
Db 181 FOYIEGEMRTRIRYNRSA 199

## RESULT 4

US-07-988-430-1  
; Sequence 1, Application US/07988430  
; Patent No. 5416202  
; GENERAL INFORMATION:  
; APPLICANT: Bernhard, Susan L.  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroli, Stephen F.  
; APPLICANT: Lane, Julie A.  
; APPLICANT: Lei, Shau-Ping  
; TITLE OF INVENTION: Materials Comprising and Methods of  
; Preparation and Use for Ribosome-Inactivating Proteins  
; TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins  
; NUMBER OF SEQUENCES: 101  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSER: Bicknell  
; STREET: Two First National Plaza, 20 South Clark  
; STREET: Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/988,430  
; FILING DATE: 19921209  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5416202and, Greta E.  
; REGISTRATION NUMBER: 35302  
; REFERENCE/DOCKET NUMBER: 31133  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 346-5750  
; TELEFAX: (312) 984-9740  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 267 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-988-430-1

Query Match 99.5%; Score 1024; DB 1; Length 267;  
Best Local Similarity 100.0%; Pred. No. 8.3e-112;  
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHIEPVLNVRVGLPINQRFILV 61  
Db 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHIEPVLNVRVGLPINQRFILV 60  
QY 62 ELSNHAELSVTLLADVNTAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDVQNRYYTFAFG 121  
Db 61 ELSNHAELSVTLLADVNTAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDVQNRYYTFAFG 120

QY 122 GNYDRLEQAGNLENIELGNGLPLEEALISALYYSTGTQTLPTLARSFICQMISEAAR 181  
Db 121 GNYDRLEQAGNLENIELGNGLPLEEALISALYYSTGTQTLPTLARSFICQMISEAAR 180  
QY 182 FOYIEGEMRTRIRYNRSA 200  
Db 181 FOYIEGEMRTRIRYNRSA 199

## RESULT 5

US-08-425-336-1  
; Sequence 1, Application US/08425336  
; Patent No. 5621083  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroli, Stephen F.  
; APPLICANT: Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; NUMBER OF SEQUENCES: 140  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/425,336  
; FILING DATE: 18-APR-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/064,691  
; FILING DATE: 12-MAY-1993  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meyers, Thomas C.  
; REGISTRATION NUMBER: P-36,989  
; REFERENCE/DOCKET NUMBER: 31394  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 267 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-425-336-1

Query Match 99.5%; Score 1024; DB 1; Length 267;  
Best Local Similarity 100.0%; Pred. No. 8.3e-112;  
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHIEPVLNVRVGLPINQRFILV 61  
Db 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHIEPVLNVRVGLPINQRFILV 60  
QY 62 ELSNHAELSVTLLADVNTAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDVQNRYYTFAFG 121  
Db 61 ELSNHAELSVTLLADVNTAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDVQNRYYTFAFG 120  
QY 122 GNYDRLEQAGNLENIELGNGLPLEEALISALYYSTGTQTLPTLARSFICQMISEAAR 181

Db 121 GNYDRLEQLAGNLRNIELGNGPLEEASALYYSTGGTQLPRLARSFIICQMISEAAR 180  
Qy 182 FOYIEGEMRTRIRYNRRA 200  
Db 181 FOYIEGEMRTRIRYNRRA 199

## RESULT 6

US-08-488-113B-1  
; Sequence 1, Application US/08488113B  
; Patent No. 5744580  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; TITLE OF INVENTION: Proteins  
; NUMBER OF SEQUENCES: 169  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/488,113B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/425,336  
; FILING DATE: 18-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/064,691  
; FILING DATE: 12-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/988,430  
; FILING DATE: 09-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McNicholas, Janet M.  
; REGISTRATION NUMBER: 32,918  
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
; TELEPHONE: 312/707-8889  
; TELEFAX: 312/707-9155  
; TELEX: 650 388-1248  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 267 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-488-113B-1

Query Match 99.5%; Score 1024; DB 1; Length 267;  
Best Local Similarity 100.0%; Pred. No. 8.3e-112;  
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IFPKQYPIINFTTAGATVQSYTNFRAVRGLTTGADVRHEIPVLPNVRVGLPINQRFILV 61  
Db 1 IFPKQYPIINFTTAGATVQSYTNFRAVRGLTTGADVRHEIPVLPNVRVGLPINQRFILV 60

Qy 62 ELSNHAELSVTILDVNTNAYVVGVRAGNGAYFFPHDPNQEDAEAIHTLFTDVQNRYYTFAFG 121  
Db 61 ELSNHAELSVTILDVNTNAYVVGVRAGNGAYFFPHDPNQEDAEAIHTLFTDVQNRYYTFAFG 120  
Qy 122 GNYDRLEQLAGNLRNIELGNGPLEEASALYYSTGGTQLPRLARSFIICQMISEAAR 181  
Db 121 GNYDRLEQLAGNLRNIELGNGPLEEASALYYSTGGTQLPRLARSFIICQMISEAAR 180  
Qy 182 FOYIEGEMRTRIRYNRRA 200  
Db 181 FOYIEGEMRTRIRYNRRA 199

## RESULT 7

US-08-477-484B-1  
; Sequence 1, Application US/08477484B  
; Patent No. 5756699  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; TITLE OF INVENTION: Proteins  
; NUMBER OF SEQUENCES: 169  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/477,484B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/425,336  
; FILING DATE: 18-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/064,691  
; FILING DATE: 12-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/988,430  
; FILING DATE: 09-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McNicholas, Janet M.  
; REGISTRATION NUMBER: 32,918  
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A  
; TELEPHONE: 312/707-8889  
; TELEFAX: 312/707-9155  
; TELEX: 650 388-1248  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 267 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-477-484B-1

Query Match 99.5%; Score 1024; DB 1; Length 267;

Best Local Similarity 100.0%; Pred. No. 8.3e-112; Mismatches 0; Indels 0; Gaps 0;  
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVREHEIPVLPNVRVGLPINQRFILV 61  
Db 1 IPPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVREHEIPVLPNVRVGLPINQRFILV 60  
QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEAIHTLFTDVQNRYYTFAFG 121  
Db 61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEAIHTLFTDVQNRYYTFAFG 120  
QY 122 GNYDRLEQLAGNLRENIELGNGLPLEEAI SALLYYSYTGCTQLPTLARSFIIICQMISEAAR 181  
Db 121 GNYDRLEQLAGNLRENIELGNGLPLEEAI SALLYYSYTGCTQLPTLARSFIIICQMISEAAR 180  
QY 182 FOYIEGEMTRIRYNRRA 200  
Db 181 FOYIEGEMTRIRYNRRA 199

RESULT 8  
US-08-646-360-1  
; Sequence 1, Application US/08646360  
; Patent No. 5837491  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; NUMBER OF SEQUENCES: 173  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/646,360  
; FILING DATE: 13-MAY-1996  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PC/US94/05348  
; FILING DATE: 12-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/064,691  
; FILING DATE: 12-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/988,430  
; FILING DATE: 09-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McNicholas, Janet M.  
; REGISTRATION NUMBER: 32,918  
; REFERENCE/DOCKET NUMBER: 200-70.P4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/707-9155  
; TELEFAX: 312/707-9155  
; TELEX: 650 388-1248  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 267 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-646-360-1

Query Match 99.5%; Score 1024; DB 2; Length 267;  
Best Local Similarity 100.0%; Pred. No. 8.3e-112; Mismatches 0; Indels 0; Gaps 0;  
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVREHEIPVLPNVRVGLPINQRFILV 61  
Db 1 IPPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVREHEIPVLPNVRVGLPINQRFILV 60  
QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEAIHTLFTDVQNRYYTFAFG 121  
Db 61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEAIHTLFTDVQNRYYTFAFG 120  
QY 122 GNYDRLEQLAGNLRENIELGNGLPLEEAI SALLYYSYTGCTQLPTLARSFIIICQMISEAAR 181  
Db 121 GNYDRLEQLAGNLRENIELGNGLPLEEAI SALLYYSYTGCTQLPTLARSFIIICQMISEAAR 180  
QY 182 FOYIEGEMTRIRYNRRA 200  
Db 181 FOYIEGEMTRIRYNRRA 199

RESULT 9  
US-08-839-765-1  
; Sequence 1, Application US/08839765  
; Patent No. 6146631  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; APPLICANT: Carroll, Stephen F.  
; APPLICANT: Studnika, Gary M.  
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
; NUMBER OF SEQUENCES: 169  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
; STREET: 500 West Madison Street, 34th floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/839,765  
; FILING DATE: 15-APR-1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/425,336  
; FILING DATE: 18-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/064,691  
; FILING DATE: 12-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/988,430  
; FILING DATE: 09-DEC-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/901,707  
; FILING DATE: 19-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/787,567  
; FILING DATE: 04-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McNicholas, Janet M.  
; REGISTRATION NUMBER: 32,918  
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 267 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-839-765-1

Query Match 99.5%; Score 1024; DB 3; Length 267;  
Best Local Similarity 100.0%; Pred. NO. 8.3e-112; Indels 0; Gaps 0;  
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 IFPKQYPIINFETAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINQRFILV 61  
Db 1 IFPKQYPIINFETAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINQRFILV 60  
QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYTTFAG 121  
Db 61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYTTFAG 120  
QY 122 GNYDRLEQLAGNRELNGPLEEASALYYSTGGTQPTLARSFIIQIMISEAAR 181  
Db 121 GNYDRLEQLAGNRELNGPLEEASALYYSTGGTQPTLARSFIIQIMISEAAR 180  
QY 182 FOYIEGEMTRIRYNRRA 200  
Db 181 FOYIEGEMTRIRYNRRA 199

## RESULT 10

US-09-136-389-1  
Sequence 1, Application US/09136389  
Patent No. 6146850  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/136,389  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/646,360  
FILING DATE: 13-MAY-1996  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70.P4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 267 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-136-389-1

Query Match 99.5%; Score 1024; DB 3; Length 267;  
Best Local Similarity 100.0%; Pred. NO. 8.3e-112; Indels 0; Gaps 0;  
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 IFPKQYPIINFETAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINQRFILV 61  
Db 1 IFPKQYPIINFETAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINQRFILV 60  
QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYTTFAG 121  
Db 61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYTTFAG 120  
QY 122 GNYDRLEQLAGNRELNGPLEEASALYYSTGGTQPTLARSFIIQIMISEAAR 181  
Db 121 GNYDRLEQLAGNRELNGPLEEASALYYSTGGTQPTLARSFIIQIMISEAAR 180  
QY 182 FOYIEGEMTRIRYNRRA 200  
Db 181 FOYIEGEMTRIRYNRRA 199

## RESULT 11

US-09-610-838-1  
Sequence 1, Application US/09610838  
Patent No. 6376217  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
APPLICANT: Carroll, Stephen F.  
APPLICANT: Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating  
TITLE OF INVENTION: Proteins  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/610,838  
FILING DATE: 06-JUL-2000  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/136,389  
FILING DATE: 18-AUG-1998  
APPLICATION NUMBER: 08/646,360  
FILING DATE: 13-MAY-1996  
APPLICATION NUMBER: PCT/US94/05348

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; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US92-09487-1

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Query Match 99.5%; Score 1024; DB 4; Length 267;
Best Local Similarity 100.0%; Pred. No. 8.3e-112;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVVRHEIPVLPNVRVGLPINQRFILV 61
Db 1 IPPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVVRHEIPVLPNVRVGLPINQRFILV 60

QY 62 ELSNHAELSVTLLDVTNAYVVGVRAGNSAYFFHPDQDDEAETHLFTDVQNRVTFAG 121
Db 61 ELSNHAELSVTLLDVTNAYVVGVRAGNSAYFFHPDQDDEAETHLFTDVQNRVTFAG 120

QY 122 GNYDRLEQLAGNLRENIELNGPLBEAISALYYSTGGTQPLTARSFICIMISEAAR 181
Db 121 GNYDRLEQLAGNLRENIELNGPLBEAISALYYSTGGTQPLTARSFICIMISEAAR 180

QY 182 FOYIEGEMTRIRYNRRA 200
Db 181 FOYIEGEMTRIRYNRRA 199

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RESULT 12
PCT-US92-09487-1
; Sequence 1, Application PC/TUS9209487
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen P.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping
; TITLE OF INVENTION: Materials Comprising and Methods of
; Preparation and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09487
; FILING DATE: 19921104
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35302
; REFERENCE/DOCKET NUMBER: 31133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US92-09487-1

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Query Match 99.5%; Score 1024; DB 5; Length 267;
Best Local Similarity 100.0%; Pred. No. 8.3e-112;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVVRHEIPVLPNVRVGLPINQRFILV 61
Db 1 IPPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVVRHEIPVLPNVRVGLPINQRFILV 60

QY 62 ELSNHAELSVTLLDVTNAYVVGVRAGNSAYFFHPDQDDEAETHLFTDVQNRVTFAG 121
Db 61 ELSNHAELSVTLLDVTNAYVVGVRAGNSAYFFHPDQDDEAETHLFTDVQNRVTFAG 120

QY 122 GNYDRLEQLAGNLRENIELNGPLBEAISALYYSTGGTQPLTARSFICIMISEAAR 181
Db 121 GNYDRLEQLAGNLRENIELNGPLBEAISALYYSTGGTQPLTARSFICIMISEAAR 180

QY 182 FOYIEGEMTRIRYNRRA 200
Db 181 FOYIEGEMTRIRYNRRA 199

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RESULT 13
US-08-378-761A-27
; Sequence 27, Application US/08378761A
; Patent No. 5635384
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,761A
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 290 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-378-761A-27

Query Match 99.5%; Score 1024; DB 1; Length 290;
Best Local Similarity 100.0%; Pred. No. 9.4e-112;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPPKQYPIINFTTAGATVQSYTNFIRAVRGRLLTTGADVVRHEIPVLPNRVGLPINORFILV 61
Db 25 IPPKQYPIINFTTAGATVQSYTNFIRAVRGRLLTTGADVVRHEIPVLPNRVGLPINORFILV 84
QY 62 ELSNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDVQNYRTTFAFG 121
Db 85 ELSNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDVQNYRTTFAFG 144
QY 122 GNYDRLEQLAGNLRENIELGNGLPEEAISALYYSTGGTQTLPTLARSFIIQIMISEAAR 181
Db 145 GNYDRLEQLAGNLRENIELGNGLPEEAISALYYSTGGTQTLPTLARSFIIQIMISEAAR 204
QY 182 FOYIEGEMTRIRYNRNSA 200
Db 205 FOYIEGEMTRIRYNRNSA 223

RESULT 14
US-08-485-286-27
; Sequence 27, Application US/08485286
; Patent No. 5646026
; Patent No. 5646026 5646119
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESS: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,286
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/378761
; FILING DATE: 26-JAN-1995
```

```
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 290 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-485-286-27
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Query Match 99.5%; Score 1024; DB 1; Length 290;
Best Local Similarity 100.0%; Pred. No. 9.4e-112;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPPKQYPIINFTTAGATVQSYTNFIRAVRGRLLTTGADVVRHEIPVLPNRVGLPINORFILV 61
Db 25 IPPKQYPIINFTTAGATVQSYTNFIRAVRGRLLTTGADVVRHEIPVLPNRVGLPINORFILV 84
QY 62 ELSNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDVQNYRTTFAFG 121
Db 85 ELSNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDVQNYRTTFAFG 144
QY 122 GNYDRLEQLAGNLRENIELGNGLPEEAISALYYSTGGTQTLPTLARSFIIQIMISEAAR 181
Db 145 GNYDRLEQLAGNLRENIELGNGLPEEAISALYYSTGGTQTLPTLARSFIIQIMISEAAR 204
QY 182 FOYIEGEMTRIRYNRNSA 200
Db 205 FOYIEGEMTRIRYNRNSA 223
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RESULT 15
5248606-4
; Patent No. 5248606
; APPLICANT: WALSH, TERENCE A.; HEY, TIMOTHY D.; MORGAN,
; ALICE E.R.
; TITLE OF INVENTION: DNA ENCODING INACTIVE PRECURSOR AND
; ACTIVE FORMS OF MAIZE RIBOSOME INACTIVATIN
; NUMBER OF SEQUENCES: 49
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/535,636
; FILING DATE: 11-JUN-1990
; SEQ ID NO: 4:
; LENGTH: 290
5248606-4
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Query Match 99.5%; Score 1024; DB 6; Length 290;
Best Local Similarity 100.0%; Pred. No. 9.4e-112;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPPKQYPIINFTTAGATVQSYTNFIRAVRGRLLTTGADVVRHEIPVLPNRVGLPINORFILV 61
Db 25 IPPKQYPIINFTTAGATVQSYTNFIRAVRGRLLTTGADVVRHEIPVLPNRVGLPINORFILV 84
QY 62 ELSNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDVQNYRTTFAFG 121
Db 85 ELSNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDVQNYRTTFAFG 144
QY 122 GNYDRLEQLAGNLRENIELGNGLPEEAISALYYSTGGTQTLPTLARSFIIQIMISEAAR 181
Db 145 GNYDRLEQLAGNLRENIELGNGLPEEAISALYYSTGGTQTLPTLARSFIIQIMISEAAR 204
QY 182 FOYIEGEMTRIRYNRNSA 200
Db 205 FOYIEGEMTRIRYNRNSA 223
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Search completed: February 10, 2004, 16:29:35

Sun Feb 15 07:29:55 2004

us-10-083-336a-10.rai

Page 9

Job time : 12.5641 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:26:46 ; Search time 25.7969 Seconds  
(without alignments)  
1623.314 Million cell updates/sec

Title: US-10-083-336A-10  
Perfect score: 1029  
Sequence: 1 MIFPKQYPIINFTTAGATVQ.....RFQYIEGEMRTRIRYNRRA 200

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/prodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/prodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/prodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/prodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/prodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/prodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/prodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/prodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/prodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/prodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/prodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/prodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/prodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/prodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/prodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/prodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/prodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/prodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1029	100.0	200	12	US-10-083-336A-10
2	1025	99.6	199	12	US-10-083-336A-5
3	1024	99.5	267	12	US-10-127-890-1
4	1024	99.5	576	12	US-10-083-336A-1
5	1020	99.1	198	12	US-10-083-336A-3
6	1014	98.5	267	12	US-10-282-935-1
7	1014	98.5	267	12	US-10-440-796-1
8	1010	98.2	198	12	US-10-083-336A-7
9	960	93.3	190	12	US-10-083-336A-11
10	956	92.9	189	12	US-10-083-336A-6
11	951	92.4	188	12	US-10-083-336A-4
12	941	91.4	188	12	US-10-083-336A-8
13	934.5	90.8	185	12	US-10-083-336A-9
14	748	72.7	179	12	US-10-083-336A-2
15	342	33.2	247	10	US-09-792-793A-39

16	342	33.2	247	12	US-10-127-890-6	Sequence 6, Appli
17	342	33.2	247	12	US-10-375-209A-39	Sequence 39, Appl
18	342	33.2	289	12	US-10-280-679B-4	Sequence 4, Appli
19	323.5	31.4	251	12	US-10-282-935-3	Sequence 3, Appli
20	323.5	31.4	251	12	US-10-440-796-3	Sequence 3, Appli
21	312	30.3	247	10	US-09-792-793A-34	Sequence 34, Appli
22	312	30.3	247	12	US-10-375-209A-34	Sequence 34, Appli
23	279	27.1	263	12	US-10-127-890-4	Sequence 4, Appli
24	277	26.9	263	12	US-10-127-890-7	Sequence 7, Appli
25	276	26.8	252	9	US-09-347-064-2	Sequence 2, Appli
26	276	26.8	252	9	US-09-347-064-8	Sequence 8, Appli
27	267.5	26.0	248	12	US-10-127-890-5	Sequence 5, Appli
28	249.5	24.2	251	12	US-10-127-890-110	Sequence 110, App
29	249.5	24.2	251	12	US-10-127-890-111	Sequence 111, App
30	248.5	24.1	251	12	US-10-127-890-101	Sequence 101, App
31	247.5	24.1	251	12	US-10-127-890-99	Sequence 99, Appl
32	247.5	24.1	251	12	US-10-127-890-107	Sequence 107, App
33	246.5	24.0	251	12	US-10-127-890-100	Sequence 100, App
34	246.5	24.0	251	12	US-10-127-890-106	Sequence 106, App
35	245.5	23.9	251	9	US-09-765-527-247	Sequence 247, App
36	245.5	23.9	251	12	US-10-127-890-2	Sequence 2, Appli
37	245.5	23.9	251	12	US-10-127-890-102	Sequence 102, App
38	245.5	23.9	251	12	US-10-127-890-103	Sequence 103, App
39	245.5	23.9	251	12	US-10-127-890-104	Sequence 104, App
40	245.5	23.9	251	12	US-10-127-890-105	Sequence 105, App
41	245.5	23.9	316	12	US-10-074-596-1	Sequence 1, Appli
42	245.5	23.9	507	12	US-10-074-596-11	Sequence 11, Appl
43	244.5	23.8	293	9	US-09-765-527-259	Sequence 259, App
44	244.5	23.8	309	9	US-09-765-527-253	Sequence 253, App
45	244.5	23.8	332	9	US-09-765-527-251	Sequence 251, App

ALIGNMENTS

RESULT 1  
US-10-083-336A-10  
; Sequence 10, Application US/10083336A  
; Publication No. US20030181665A1  
; GENERAL INFORMATION:  
; APPLICANT: Olson, Mark A  
; APPLICANT: Millard, Charles B  
; APPLICANT: Byrne, Michael P  
; APPLICANT: Wannemacher, Robert W  
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof  
; FILE REFERENCE: P67452US0 (RIID 01-58)  
; CURRENT APPLICATION NUMBER: US/10/083,336A  
; CURRENT FILING DATE: 2002-05-21  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 200  
; TYPE: PRT  
; ORGANISM: Ricinus communis  
US-10-083-336A-10

Query Match	100.0%	Score	1029;	DB	12;	Length	200;
Best Local Similarity	100.0%	Pred	No. 6e-110;				
Matches	200;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	MIFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVHRHPIVLPNVRVGLPINQRFIL	60				
Db	1	MIFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVHRHPIVLPNVRVGLPINQRFIL	60				
Qy	61	VELSNHAEISVTLALDVNAYVVGVRAGNSAFFHPDNOEDAEAIHTLFTDVQNRVTFAP	120				
Db	61	VELSNHAEISVTLALDVNAYVVGVRAGNSAFFHPDNOEDAEAIHTLFTDVQNRVTFAP	120				
Qy	121	GGNYDRLEQLAGNRLNIELGNGLPEEATSAIYYSTGTQPTLARSFTICIQMISEAA	180				
Db	121	GGNYDRLEQLAGNRLNIELGNGLPEEATSAIYYSTGTQPTLARSFTICIQMISEAA	180				
Qy	181	RFQYIEGEMRTRIRYNRRA	200				

Db 181 RFQYIEGMRTRIRYNRSA 200  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,360  
FILING DATE: 13-MAY-1996  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70.P4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 267 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-127-890-1  
Query Match 99.6%; Score 1025; DB 12; Length 199;  
Best Local Similarity 100.0%; Pred. No. 1.7e-109;  
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINQRIL 60  
Db 1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINQRIL 60  
QY 61 VELSNAELSVTLALDVNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYTFAP 120  
Db 61 VELSNAELSVTLALDVNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYTFAP 120  
QY 121 GGYDRLEQLAGNREINELGNGLPEEAISALYYSTGTQTLPTLARSFIIQIMISEAA 180  
Db 121 GGYDRLEQLAGNREINELGNGLPEEAISALYYSTGTQTLPTLARSFIIQIMISEAA 180  
QY 181 RFQYIEGMRTRIRYNRSS 199  
Db 181 RFQYIEGMRTRIRYNRSS 199  
RESULT 3  
US-10-127-890-1  
Sequence 1, Application US/10127890  
Publication No. US20030166196A1  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
Carroll, Stephen F.  
Studnicka, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSER: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/127,890  
FILING DATE: 23-Apr-2002  
CLASSIFICATION: <Unknown>

QY 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINQRILV 61  
Db 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINQRILV 60  
QY 62 ELSNHAELSVTLALDVNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYTFAPG 121  
Db 61 ELSNHAELSVTLALDVNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYTFAPG 120  
QY 122 GGYDRLEQLAGNREINELGNGLPEEAISALYYSTGTQTLPTLARSFIIQIMISEAAR 181  
Db 121 GGYDRLEQLAGNREINELGNGLPEEAISALYYSTGTQTLPTLARSFIIQIMISEAAR 180  
QY 182 FOYIEGEMRTRIRYNRSA 200  
Db 181 FOYIEGEMRTRIRYNRSA 199  
RESULT 4  
US-10-083-336A-1  
Sequence 1, Application US/10083336A  
Publication No. US20030181665A1  
GENERAL INFORMATION:  
APPLICANT: Olson, Mark A  
APPLICANT: Millard, Charles B  
APPLICANT: Byrne, Michael P  
APPLICANT: Wannemacher, Robert W  
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof  
FILE REFERENCE: P67452US0 (RIID 01-58)  
CURRENT APPLICATION NUMBER: US/10/083,336A  
CURRENT FILING DATE: 2002-05-21  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 576  
TYPE: PRT  
ORGANISM: Ricinus communis  
US-10-083-336A-1  
Query Match 99.5%; Score 1024; DB 12; Length 576;

Best Local Similarity 100.0%; Pred. No. 1e-108;  
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 IPPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHIEPVLNVRVGLPINQRFILV 61  
DB 36 IPPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHIEPVLNVRVGLPINQRFILV 95  
QY 62 ELSNHAELSCTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAG 121  
DB 96 ELSNHAELSCTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAG 155  
QY 122 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQLPTLARSFIIQIMISEAAR 181  
DB 156 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQLPTLARSFIIQIMISEAAR 215  
QY 182 FOYIEGEMTRIRYNRRSA 200  
DB 216 FOYIEGEMTRIRYNRRSA 234

RESULT 5  
US-10-083-336A-3  
; Sequence 3, Application US/10083336A  
; Publication No. US20030181665A1  
; GENERAL INFORMATION:  
; APPLICANT: Olson, Mark A  
; APPLICANT: Millard, Charles B  
; APPLICANT: Byrne, Michael P  
; APPLICANT: Wannemacher, Robert W  
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof  
; FILE REFERENCE: P67452US0 (RIID 01-58)  
; CURRENT APPLICATION NUMBER: US/10/083,336A  
; CURRENT FILING DATE: 2002-05-21  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 198  
; TYPE: PRT  
; ORGANISM: Ricinus communis  
US-10-083-336A-3

Query Match 99.1%; Score 1020; DB 12; Length 198;  
Best Local Similarity 100.0%; Pred. No. 6.4e-109;  
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 IPPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHIEPVLNVRVGLPINQRFILV 61  
DB 1 IPPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHIEPVLNVRVGLPINQRFILV 60  
QY 62 ELSNHAELSCTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAG 121  
DB 61 ELSNHAELSCTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAG 120  
QY 122 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQLPTLARSFIIQIMISEAAR 181  
DB 121 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQLPTLARSFIIQIMISEAAR 180  
QY 182 FOYIEGEMTRIRYNRRS 199  
DB 181 FOYIEGEMTRIRYNRRS 198

RESULT 6  
US-10-082-935-1  
; Sequence 1, Application US/10282935  
; Publication No. US20030143193A1  
; GENERAL INFORMATION:  
; APPLICANT: VITETTA, ELLEN S.  
; APPLICANT: GHETTIE, VICTOR F.  
; APPLICANT: SMALLSHAW, JOAN  
; APPLICANT: BALUNA, ROXANA G.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF  
; PROTEINACEOUS COMPOUNDS

FILE REFERENCE: UTSD:884US  
; CURRENT APPLICATION NUMBER: US/10/282,935  
; CURRENT FILING DATE: 2002-10-29  
; PRIOR APPLICATION NUMBER: 09/538,873  
; PRIOR FILING DATE: 2000-03-30  
; PRIOR APPLICATION NUMBER: 60/126,826  
; PRIOR FILING DATE: 1999-03-30  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 267  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-10-282-935-1

Query Match 98.5%; Score 1014; DB 12; Length 267;  
Best Local Similarity 100.0%; Pred. No. 4.8e-108;  
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 PKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHIEPVLNVRVGLPINQRFILV 63  
DB 3 PKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHIEPVLNVRVGLPINQRFILV 62  
QY 64 SNHAELSCTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAG 123  
DB 63 SNHAELSCTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAG 122  
QY 124 YDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQLPTLARSFIIQIMISEAAR 183  
DB 123 YDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQLPTLARSFIIQIMISEAAR 182  
QY 184 YIEGEMTRIRYNRRSA 200  
DB 183 YIEGEMTRIRYNRRSA 199

RESULT 7  
US-10-440-796-1  
; Sequence 1, Application US/10440796  
; Publication No. US20040009148A1  
; GENERAL INFORMATION:  
; APPLICANT: VITETTA, ELLEN S.  
; APPLICANT: GHETTIE, VICTOR F.  
; APPLICANT: SMALLSHAW, JOAN  
; APPLICANT: BALUNA, ROXANA G.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK  
; FILE REFERENCE: UTSD:603  
; CURRENT APPLICATION NUMBER: US/10/440,796  
; CURRENT FILING DATE: 2003-05-19  
; PRIOR APPLICATION NUMBER: US/09/538,873  
; PRIOR FILING DATE: 2000-03-30  
; PRIOR APPLICATION NUMBER: 60/126,826  
; PRIOR FILING DATE: 1999-03-30  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 267  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-10-440-796-1

Query Match 98.5%; Score 1014; DB 12; Length 267;  
Best Local Similarity 100.0%; Pred. No. 4.8e-108;  
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 PKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHIEPVLNVRVGLPINQRFILV 63

Db 3 PKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHIEPVLNPRVGLPINQRFILVEL 62  
Qy 64 SNHAEISVTLALDVNTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNRYYTFAFGN 123  
Db 63 SNHAEISVTLALDVNTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNRYYTFAFGN 122  
Qy 124 YDRLEQLAGNLRNENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIQIMISEAARFQ 183  
Db 123 YDRLEQLAGNLRNENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIQIMISEAARFQ 182  
Qy 184 YIEGEMTRIRYNRRSA 200  
Db 183 YIEGEMTRIRYNRRSA 199

RESULT 8  
US-10-083-336A-7  
; Sequence 7, Application US/10083336A  
; Publication No. US20030181665A1  
; GENERAL INFORMATION:  
; APPLICANT: Olson, Mark A  
; APPLICANT: Millard, Charles B  
; APPLICANT: Byrne, Michael P  
; APPLICANT: Wannemacher, Robert W  
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof  
; FILE REFERENCE: P67452US0 (RIID 01-58)  
; CURRENT APPLICATION NUMBER: US/10/083,336A  
; CURRENT FILING DATE: 2002-05-21  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 198  
; TYPE: PRT  
; ORGANISM: Ricinus communis  
US-10-083-336A-7

Query Match 98.2%; Score 1010; DB 12; Length 198;  
Best Local Similarity 100.0%; Pred. No. 9.1e-108;  
Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 4 PKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHIEPVLNPRVGLPINQRFILVEL 63  
Db 3 PKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHIEPVLNPRVGLPINQRFILVEL 62  
Qy 64 SNHAEISVTLALDVNTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNRYYTFAFGN 123  
Db 63 SNHAEISVTLALDVNTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNRYYTFAFGN 122  
Qy 124 YDRLEQLAGNLRNENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIQIMISEAARFQ 183  
Db 123 YDRLEQLAGNLRNENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIQIMISEAARFQ 182  
Qy 184 YIEGEMTRIRYNRRS 199  
Db 183 YIEGEMTRIRYNRRS 198

RESULT 9  
US-10-083-336A-11  
; Sequence 11, Application US/10083336A  
; Publication No. US20030181665A1  
; GENERAL INFORMATION:  
; APPLICANT: Olson, Mark A  
; APPLICANT: Millard, Charles B  
; APPLICANT: Byrne, Michael P  
; APPLICANT: Wannemacher, Robert W  
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof  
; FILE REFERENCE: P67452US0 (RIID 01-58)  
; CURRENT APPLICATION NUMBER: US/10/083,336A  
; CURRENT FILING DATE: 2002-05-21  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 11  
; LENGTH: 190  
; TYPE: PRT  
; ORGANISM: Ricinus communis  
US-10-083-336A-11

Query Match 93.3%; Score 960; DB 12; Length 190;  
Best Local Similarity 95.0%; Pred. No. 4.8e-102;  
Matches 190; Conservative 0; Mismatches 0; Indels 10; Gaps 1;  
Qy 1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHIEPVLNPRVGLPINQRFIL 60  
Db 1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHIEPVLNPRVGLPINQRFIL 50  
Qy 61 VELSNHAEISVTLALDVNTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNRYYTFAF 120  
Db 51 VELSNHAEISVTLALDVNTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNRYYTFAF 110  
Qy 121 GGNVDRLEQLAGNLRNENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIQIMISEAA 180  
Db 111 GGNVDRLEQLAGNLRNENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIQIMISEAA 170  
Qy 181 RFQYIEGEMTRIRYNRRSA 200  
Db 171 RFQYIEGEMTRIRYNRRSA 190

RESULT 10  
US-10-083-336A-6  
; Sequence 6, Application US/10083336A  
; Publication No. US20030181665A1  
; GENERAL INFORMATION:  
; APPLICANT: Olson, Mark A  
; APPLICANT: Millard, Charles B  
; APPLICANT: Byrne, Michael P  
; APPLICANT: Wannemacher, Robert W  
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof  
; FILE REFERENCE: P67452US0 (RIID 01-58)  
; CURRENT APPLICATION NUMBER: US/10/083,336A  
; CURRENT FILING DATE: 2002-05-21  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 189  
; TYPE: PRT  
; ORGANISM: Ricinus communis  
US-10-083-336A-6

Query Match 92.9%; Score 956; DB 12; Length 189;  
Best Local Similarity 95.0%; Pred. No. 1.4e-101;  
Matches 189; Conservative 0; Mismatches 0; Indels 10; Gaps 1;  
Qy 1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHIEPVLNPRVGLPINQRFIL 60  
Db 1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHIEPVLNPRVGLPINQRFIL 50  
Qy 61 VELSNHAEISVTLALDVNTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNRYYTFAF 120  
Db 51 VELSNHAEISVTLALDVNTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNRYYTFAF 110  
Qy 121 GGNVDRLEQLAGNLRNENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIQIMISEAA 180  
Db 111 GGNVDRLEQLAGNLRNENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIQIMISEAA 170  
Qy 181 RFQYIEGEMTRIRYNRRS 199  
Db 171 RFQYIEGEMTRIRYNRRS 189

RESULT 11  
US-10-083-336A-4  
; Sequence 4, Application US/10083336A  
; Publication No. US20030181665A1

```

; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-4

Query Match      92.4%; Score 951; DB 12; Length 188;
Best Local Similarity 94.9%; Pred. No. 5.1e-101;
Matches 188; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINQRFILV 61
DB 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILV 50
QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAFG 121
DB 51 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAFG 110
QY 122 GNYDRLEQAGNLRENIELGNGLPGLPEEALISALYYSTGGTQTLPTLARSFIIQIMISEAAR 181
DB 111 GNYDRLEQAGNLRENIELGNGLPGLPEEALISALYYSTGGTQTLPTLARSFIIQIMISEAAR 170
QY 182 FOYIEGEMRTRIRYNRRS 199
DB 171 FOYIEGEMRTRIRYNRRS 188

RESULT 12
US-10-083-336A-8
; Sequence 8, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-8

Query Match      91.4%; Score 941; DB 12; Length 188;
Best Local Similarity 94.9%; Pred. No. 7.2e-100;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 4 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINQRFILVEL 63
DB 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 52
QY 64 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAFGN 123
DB 53 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAFGN 112
QY 124 YDRLEQAGNLRENIELGNGLPGLPEEALISALYYSTGGTQTLPTLARSFIIQIMISEAARFQ 183
DB 124 YDRLEQAGNLRENIELGNGLPGLPEEALISALYYSTGGTQTLPTLARSFIIQIMISEAARFQ 173

; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-9

Query Match      90.8%; Score 934.5; DB 12; Length 185;
Best Local Similarity 93.4%; Pred. No. 3.9e-99;
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINQRFILV 61
DB 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINQRFILV 47
QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAFG 121
DB 48 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAFG 107
QY 122 GNYDRLEQAGNLRENIELGNGLPGLPEEALISALYYSTGGTQTLPTLARSFIIQIMISEAAR 181
DB 108 GNYDRLEQAGNLRENIELGNGLPGLPEEALISALYYSTGGTQTLPTLARSFIIQIMISEAAR 167
QY 182 FOYIEGEMRTRIRYNRRS 199
DB 168 FOYIEGEMRTRIRYNRRS 185

RESULT 14
US-10-083-336A-2
; Sequence 2, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-2

Query Match      72.7%; Score 748; DB 12; Length 179;
Best Local Similarity 100.0%; Pred. No. 1e-77;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: February 10, 2004, 16:53:55  
Job time : 26.7969 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2004, 16:17:35 ; Search time 10.8228 Seconds  
(without alignments)  
1777.145 Million cell updates/sec

Title: US-10-083-336A-10

Perfect score: 1029

Sequence: 1 MPPKQYPIINFATTAGATVQ.....RFQYIEGEMTRIRYNRSA 200

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 76:\*

1: Pir1:\*

2: Pir2:\*

3: Pir3:\*

4: Pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1024	99.5	576	1 RLCSD	ricin D precursor
2	934.5	90.8	564	1 RUCSAG	agglutinin precursor
3	353.5	34.4	528	2 S32431	abrin-d precursor
4	353.5	34.4	562	2 S16022	abrin-c precursor
5	345	33.5	527	2 S32430	abrin-b precursor
6	342	33.2	289	1 RLTTZT	rRNA N-glycosidase
7	338	32.8	247	2 JU0393	karasurin - Mongol
8	338	32.8	247	2 JU0392	karasurin-B - Tric
9	338	32.8	289	2 JU0506	karasurin C - Tric
10	336.5	32.7	251	2 C39761	abrin (clone 7.2)
11	329.5	32.0	528	1 T2LSA	abrin-a precursor
12	307.5	29.9	278	2 S23519	beta-luffin - smoo
13	300.5	29.2	250	2 UN0108	luffin-b - smooth
14	291	28.3	570	2 S62627	agglutinin I precu
15	286	27.8	254	2 PD0018	mistletoe lectin I
16	284.5	27.6	277	2 S24494	rRNA N-glycosidase
17	279	27.1	286	2 S25560	rRNA N-glycosidase
18	277	27.0	245	2 JU0480	rRNA N-glycosidase
19	277	26.9	286	1 RUPUGG	rRNA N-glycosidase
20	272	26.4	286	2 JU0435	rRNA N-glycosidase
21	245.5	23.9	316	2 JU0753	rRNA N-glycosidase
22	197.5	19.2	294	2 S28421	rRNA N-glycosidase
23	182	17.7	313	2 S17757	rRNA N-glycosidase
24	180.5	17.5	261	2 JU0401	antiviral protein
25	178	17.3	278	2 A39817	rRNA N-glycosidase
26	156	15.2	272	2 JU0481	betavulgan - beet
27	149.5	14.5	289	2 T12573	rRNA N-glycosidase
28	140	13.6	280	1 RLBH	rRNA N-glycosidase
29	137	13.3	275	2 S36331	tritin - wheat

## ALIGNMENTS

## RESULT 1

## RLCSD

ricin D precursor - castor bean

N;Contains: rRNA N-glycosidase (EC 3.2.2.22)

C;Species: Ricinus communis (castor bean)

C;Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text\_change 16-Jul-1999

C;Accession: A24041; S20513; A24614; A03372; A24010; A03374; S10903

R;Halling, K.C.; Halling, A.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F.

Nucleic Acids Res. 13, 8019-8033, 1985

A;Title: Genomic cloning and characterization of a ricin gene from Ricinus communis.

A;Reference number: A24041; MUID:86067214; PMID:2999712

A;Accession: A24041

A;Molecule type: DNA

A;Residues: 1-576 <HAL>

A;Cross-references: GB:X03179; NID:g21082; PIDN:CAA26939.1; PID:g21083

R;Tregear, J.M.; Roberts, L.M.

Plant Mol. Biol. 18, 515-525, 1992

A;Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene

A;Reference number: S20513; MUID:92163016; PMID:1371405

A;Accession: S20513

A;Molecule type: DNA

A;Residues: 1-576 <TR>

A;Cross-references: EMBL:X52908; NID:g21084; PIDN:CAA37095.1; PID:g21085

R;Lamb, F.I.; Roberts, L.M.; Lord, J.M.

Eur. J. Biochem. 148, 285-270, 1985

A;Title: Nucleotide sequence of cloned cDNA coding for preprorin.

A;Reference number: A24614; MUID:85179479; PMID:3838723

A;Accession: A24614

A;Molecule type: mRNA

A;Residues: 12-75, 'D', 77-550, 'R', 552-576 <LAM>

A;Cross-references: GB:X02388; NID:g21077; PIDN:CAA26230.1; PID:g21078

R;Yoshitake, S.; Funatsu, G.; Funatsu, M.

Agric. Biol. Chem. 42, 1267-1274, 1978

A;Title: Isolation and sequences of peptic peptides, and the complete sequence of the

A;Reference number: A03372

A;Accession: A03372

A;Molecule type: protein

A;Residues: 36-97, 'Q', 99-109, 'S', 111-269, 'D', 272-283, 'L', 285-288, 290-302 <YOS>

A;Note: this paper cites the others in the series providing experimental details for the

R;Araki, T.; Funatsu, G.

FEBS Lett. 191, 121-124, 1985

A;Title: Revised amino acid sequence of the B-chain of ricin D due to loss of tryptophan

A;Reference number: A24010

A;Accession: A24010

A;Molecule type: protein

A;Residues: 315-383, 'PS', 386-576 <ARA>

R;Funatsu, G.; Kimura, M.; Funatsu, M.

Agric. Biol. Chem. 43, 2221-2224, 1979

A;Title: Primary structure of Ala chain of ricin D.

A;Reference number: A03374

A;Accession: A03374

A;Molecule type: protein

A;Molecule type: protein

A;Residues: 315-335,'N',337-342,'NH',345-362,364-383,'PS',386-399,'T',401,'D',403,'E',40527,'E',529-564,'W',566,'H',567-570,'LI',573-574,'F' <FUN>  
A;Note: this paper, one of a series, summarizes the experimental details for the determination of the complete amino acid sequence of the B-chain of the Ricinus communis agglutinin.  
R;Ready, M.P.; Kim, Y.; Robertus, J.D.  
Proteins 10, 270-278, 1991  
A;Title: Site-directed mutagenesis of ricin A-chain and implications for the mechanism of ricin toxicity.  
A;Reference number: A48237; PMID:91352006; PMID:1881883  
A;Contents: annotation; active site  
R;Rutenber, E.; Robertus, J.D.  
Proteins 10, 260-269, 1991  
A;Title: Structure of ricin B-chain at 2.5 angstrom resolution.  
A;Reference number: A48238; PMID:91352005; PMID:1881882  
A;Contents: annotation; X-ray crystallography, 2.5 angstroms  
R;Katzin, B.J.; Collins, E.J.; Robertus, J.D.  
Proteins 10, 251-259, 1991  
A;Title: Structure of ricin A-chain at 2.5 angstroms.  
A;Reference number: A48239; PMID:91352004; PMID:1881881  
A;Contents: annotation; X-ray crystallography, 2.5 angstroms  
C;Comment: The functional molecule is a disulfide-linked dimer of A and B chains, which into the cell of the A chain; B chains are also responsible for cell agglutination (lectin).  
C;Comment: This protein is cytotoxic and very poisonous to animals.  
C;Superfamily: ricin; rRNA N-glycosidase homology  
C;Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed  
F;1-35/Domain: signal sequence #status predicted <SIG>  
F;36-302/Product: ricin D chain A #status experimental <ACH>  
F;46-293/Domain: rRNA N-glycosidase homology <RNG>  
F;315-576/Product: ricin D chain B #status experimental <BCH>  
F;331-373,374-414,417-455,462-497,501-540,543-576/Region: 40-residue repeats  
F;45,409,449/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F;115,158,243,244/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted  
F;212/Active site: Glu #status experimental  
F;215/Active site: Arg #status predicted  
F;294,318,334-353,377-394,465-478,504-521/Disulfide bonds: #status experimental  
F;336,349,360/Binding site: N-acetyl-galactosamine (Asp, Gln, Asn) #status experimental  
F;548,569/Binding site: N-acetyl-galactosamine (Asp, Asn) #status experimental

Query Match 99.5%; Score 1024; DB 1; Length 576;  
Best Local Similarity 100.0%; Pred. No. 2,1e-84; Indels 0; Gaps 0;  
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFPKQYPIINFITAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNVRVGLPINORFVLV 61  
DB 36 IFPKQYPIINFITAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNVRVGLPINORFVLV 95

QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAG 121  
DB 96 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAG 155

QY 122 GNYDRLEQLAGNREINELGNGLPEEAISALYYSTGTQPTLARSFLICQMISEAAR 181  
DB 156 GNYDRLEQLAGNREINELGNGLPEEAISALYYSTGTQPTLARSFLICQMISEAAR 215

QY 182 FOYIEGEMTRIRYNRRA 200  
DB 216 FOYIEGEMTRIRYNRRA 234

RESULT 2  
RLCSAG  
agglutinin precursor - castor bean  
N;Contains: Ricinus communis (castor bean)  
C;Species: Ricinus communis  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 16-Jul-1999  
C;Accession: A24261; A24210  
R;Roberts, L.M.; Lamb, I.F.; Pappin, D.J.C.; Lord, J.M.  
J. Biol. Chem. 260, 15692-15696, 1985  
A;Title: The primary sequence of Ricinus communis agglutinin. Comparison with ricin.  
A;Reference number: A24261; PMID:86059449; PMID:2999130  
A;Accession: A24261  
A;Molecule type: mRNA  
A;Residues: 1-564 <ROB>  
A;Cross-references: GB:M12089; NID:g169700; PID:AAA33869.1; PID:g169701

R;Araki, T.; Yoshioka, Y.; Funatsu, G.  
Biochim. Biophys. Acta 872, 277-285, 1986  
A;Title: The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin.  
A;Reference number: A24210  
A;Accession: A24210  
A;Molecule type: protein  
A;Residues: 303-325,'F',327-330,'T',332-361,'D',363-373,'G',375-403,'T',405-551,'V',553-557,'E',529-564,'W',566,'H',567-570,'LI',573-574,'F' <FUN>  
C;Comment: This protein has strong agglutinating activity and weak cytotoxicity compared to ricin.  
C;Superfamily: ricin; rRNA N-glycosidase homology  
C;Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed  
F;1-24/Domain: signal sequence #status predicted <SIG>  
F;25-290/Product: agglutinin chain A #status predicted <ACH>  
F;35-281/Domain: rRNA N-glycosidase homology <RNG>  
F;303-564/Product: agglutinin chain B #status experimental <BCH>  
F;319-361,362-402,405-443,450-485,489-528,531-564/Region: 40-residue repeats  
F;334,259/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;104,147,231,232/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted  
F;200,203/Active site: Glu, Arg #status predicted  
F;282-306,322-341,365-382,453-466,492-509/Disulfide bonds: #status predicted  
F;324,337,348/Binding site: N-acetyl-galactosamine (Asp, Gln, Asn) #status predicted  
F;397,437/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F;536,557/Binding site: N-acetyl-galactosamine (Asp, Asn) #status predicted

Query Match 90.8%; Score 934.5; DB 1; Length 564;  
Best Local Similarity 92.0%; Pred. No. 2.4e-76; Indels 1; Gaps 1;  
Matches 183; Conservative 7; Mismatches 8; Indels 1; Gaps 1;

QY 2 IFPKQYPIINFITAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNVRVGLPINORFVLV 61  
DB 25 IFPKQYPIINFITAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNVRVGLPINORFVLV 84

QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAG 121  
DB 85 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAG 144

QY 122 GNYDRLEQLAGNREINELGNGLPEEAISALYYSTGTQPTLARSFLICQMISEAAR 181  
DB 145 GNYDRLEQLAGNREINELGNGLPEEAISALYYSTGTQPTLARSFLICQMISEAAR 203

QY 182 FOYIEGEMTRIRYNRRA 200  
DB 204 FOYIEGEMTRIRYNRRA 222

RESULT 3  
S32431  
abrin-d precursor - Indian licorice (fragment)  
N;Contains: rRNA N-glycosidase (EC 3.2.2.22)  
C;Species: Abrus precatorius (Indian licorice)  
C;Date: 30-Sep-1993 #sequence\_revision 01-Aug-1997 #text\_change 01-Aug-1997  
C;Accession: S32431; S34408  
R;Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.  
J. Mol. Biol. 229, 263-267, 1993  
A;Title: Primary structure of three distinct isoabrinins determined by cDNA sequencing.  
A;Reference number: S32429; PMID:93132798; PMID:8421313  
A;Accession: S32431  
A;Molecule type: mRNA  
A;Residues: 1-528 <HUN>  
A;Cross-references: GB:M98346  
R;Hung, C.; Lee, M.; Lee, T.; Lin, J.  
Submitted to the EMBL Data Library, March 1993  
A;Reference number: S34408  
A;Accession: S34408  
A;Molecule type: mRNA  
A;Residues: 1-169,'C',171-320,'L',322-528 <HUN>  
A;Cross-references: GB:M98346  
C;Comment: Abrin consists of an A chain, which inhibits protein synthesis by inactivating the A and B chains are linked by a single disulfide bond, which is essential for toxicity.  
C;Superfamily: ricin; rRNA N-glycosidase homology  
C;Keywords: disulfide bond, duplication; glycoprotein; glycosidase; hydrolase; lectin; P  
F;1-251/Product: abrin-d chain A #status predicted <ACH>  
F;7-246/Domain: rRNA N-glycosidase homology <RNG>  
F;261-528/Product: abrin-d chain B #status predicted <BCH>





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Best Local Similarity   39.5%;   Pred.No. 2.6e-23;
Matches    73; Conservative   46; Mismatches    54; Indels    12; Gaps     5;

QY      10 INFTTAGATVQSNTNFIRAVRGRLLTTGADVRHEIPVLPNRVGLPINORFILVELSNHAEL 69
       :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db      25 VGFRLSGATSSSYGVFISNLRKALPNERKL-YDIPLL--RSSLPGSQRVALIHITNYADE 81

QY      70 SVTLALDVNTAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTTFAFGGNYDRLE 128
       ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db      82 TTSVAIDVTNVIMGYRAGDTSYFF---NEASATEAAKVYFKDAKRKVTLPYSGNYERLQ 138

QY      129 QLAGNLRENIETLNGPLEEAIISALYYYSCTGTQLPTLARSFFIICIMISEAARFOYIEGE 188
       :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db      139 TAAGKIRENIPGLPALDSAITTLFYNNAN----SAASALMWLIQTSEAAARYKFIEQQ 193

QY      189 MRTRI 193
       :|::
Db      194 IGKRV 198

RESULT 7
JUO393
Karasurin - Mongolian snake-gourd
C:Species: Trichosanthes kirilowii (Mongolian snake-gourd)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 12-Apr-1995
C:Accession: JUO393; PS0163
R:Toyokawa, S.; Takeda, T.; Kato, Y.; Wakabayashi, K.; Ogiwara, Y.
Chem. Pharm. Bull. 39, 1244-1249, 1991
A:title: The complete amino acid sequence of an abortifacient protein, karasuriin
A:Reference number: JUO393; MUID:92005921; PMID:1914000
A:Accession: JUO393
A:Molecule type: protein
A:Residues: 1-247 <TOY>
A>Note: a sequence which lacks Ala-247 is also shown in this publication
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C:Keywords: abortifacient
F;4-243/Domain: rRNA N-glycosidase homology <RMG>

Query Match          32.8%; Score 338; DB 2; Length 247;
Best Local Similarity 40.0%; Pred. No. 4.8e-23;
Matches    74; Conservative   46; Mismatches    53; Indels    12; Gaps     5;

QY      10 INTTAGATVQSNTNFIRAVRGRLLTTGADVRHEIPVLPNRVGLPINORFILVELSNHAEL 69
Db      2 VSPFLSGATSSSYGVFISNLRKALPYERKL-YDIPLL--RSTUPGSQRVALIHITNYADE 58

QY      70 SVTLALDVNTAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTTFAFGGNYDRLE 128
Db      59 TTSVAIDVTNVIMGYRAGDTSYFF---NEASATEAAKVYFKDAKRKVTLPYSGNYERLQ 115

QY      129 QLAGNLRENIETLNGPLEEAIISALYYYSCTGTQLPTLARSFFIICIMISEAARFOYIEGE 188
Db      116 IAAGKIRENIPGLPALDSAITTLFYNNAN----SAASALMWLIQTSEAAARYKFIEQQ 170

QY      189 MRTRI 193
Db      171 IGKRV 175

RESULT 8
JC5032
karasurin-B - Trichosanthes kirilowii var. japonica
C:Species: Trichosanthes kirilowii var. japonica
C>Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 23-May-1997
C:Accession: JC5032
R:Kondo, T.; Mizukami, H.; Takeda, T.; Ogiwara, Y.
Biol. Pharm. Bull. 19, 1485-1489, 1996
A:title: Amino acid sequences and ribosome-inactivating activities of karasurins
A:Reference number: JC5032; MUID:97108848; PMID:8951169
A:Accession: JC5032
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-247 <KON>
```

C;Comment: This protein belongs to type I ribosomal-inactivating proteins which catalyze  
 C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology  
 F;4-243/Domain: rRNA N-glycosidase homology <RNG>

Query Match 32.8%; Score 338; DB 2; Length 247;  
 Best Local Similarity 40.0%; Pred. No. 4.8e-23;  
 Matches 74; Conservative 46; Mismatches 53; Indels 12; Gaps 5;

QY 10 INFTAGATVQSYTNFIRAVRGRLTGDVREHPIVLPNVRGLPINQRFILVELSNHAEI 69  
 Db 2 VSRUGATSSSGVFSINRKPVERKL-YDIPLL--RSTLPQSQRVALIHLTNVADE 58  
 QY 70 SVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDA-EAITHLFTDQVNRYYTAFGGNYDRLE 128  
 Db 59 TISVAIDVTNVVGMVRAGDTSYFF--NEASATEAAKYVFKDKRKVTLPYSGNYERLQ 115  
 QY 129 QLAGNRENIELNGPLEAISAALYVYSGTGTLPRLARSFIIQIMISEARFQVIEG 188  
 Db 116 IAAGKIRENIPGLPALDSAITTLFYNNAN-----SAASALMVLIIQSTSEAAKYFIEQ 170  
 QY 189 MRTRI 193  
 Db 171 IGRV 175

## RESULT 9

karasurin C - Trichosanthes kirilowii var. japonica  
 N;Contains: karasurin A  
 C;Species: Trichosanthes kirilowii var. japonica  
 C;Date: 23-Sep-1997 #sequence\_revision 23-Sep-1997 #text\_change 19-Jul-2002  
 C;Accession: JC5606; JC5033  
 R;Mizukami, H.; Iida, K.; Kondo, T.; Ogiwara, Y.  
 Biol. Pharm. Bull. 20, 711-713, 1997  
 A;Title: Cloning and bacterial expression of a gene encoding ribosome-inactivating prote  
 A;Reference number: JC5606; MUID:97356562; PMID:9212998  
 A;Accession: JC5606  
 A;Molecule type: DNA  
 A;Residues: 1-289 <MTZ>  
 A;Cross-references: DDBJ:AB000666; NID:92329830; PIDN:BAA21786.1; PID:92329831  
 R;Kondo, T.; Mizukami, H.; Takeda, T.; Ogiwara, Y.  
 Biol. Pharm. Bull. 19, 1485-1489, 1996  
 A;Title: Amino acid sequences and ribosome-inactivating activities of karasurin-B and ka  
 A;Reference number: JC5032; MUID:97108948; PMID:8951169  
 A;Accession: JC5033  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 22-270 <KON>

C;Comment: This protein is a ribosome-inactivating protein and exhibit cytotoxic, aborti  
 C;Comment: This protein belongs to type I ribosomal-inactivating proteins which catalyze  
 C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology  
 F;22-270/Product: karasurin C #status predicted <MAC>  
 F;24-270/Product: karasurin A #status predicted <MAA>  
 F;27-266/Domain: rRNA N-glycosidase homology <RNG>

Query Match 32.8%; Score 338; DB 2; Length 289;  
 Best Local Similarity 40.0%; Pred. No. 5.9e-23;  
 Matches 74; Conservative 46; Mismatches 53; Indels 12; Gaps 5;

QY 10 INFTAGATVQSYTNFIRAVRGRLTGDVREHPIVLPNVRGLPINQRFILVELSNHAEI 69  
 Db 25 VSRUGATSSSGVFSINRKPVERKL-YDIPLL--RSTLPQSQRVALIHLTNVADE 81  
 QY 70 SVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDA-EAITHLFTDQVNRYYTAFGGNYDRLE 128  
 Db 82 TISVAIDVTNVVGMVRAGDTSYFF--NEASATEAAKYVFKDKRKVTLPYSGNYERLQ 138  
 QY 129 QLAGNRENIELNGPLEAISAALYVYSGTGTLPRLARSFIIQIMISEARFQVIEG 188  
 Db 139 IAAGKIRENIPGLPALDSAITTLFYNNAN-----SAASALMVLIIQSTSEAAKYFIEQ 193  
 QY 189 MRTRI 193

Db 194 IGRV 198

## RESULT 10

C39761  
 abrin (clone 7.2) precursor - Indian licorice (fragment)  
 N;Contains: rRNA N-glycosidase (EC 3.2.2.22)  
 C;Species: Abrus precatorius (Indian licorice)  
 C;Date: 21-Feb-1992 #sequence\_revision 31-Dec-1993 #text\_change 20-Aug-1999  
 C;Accession: C39761; S14471  
 R;Evensen, G.; Mathiesen, A.; Sundan, A.  
 J. Biol. Chem. 266, 6848-6852, 1991  
 A;Title: Direct molecular cloning and expression of two distinct abrin A-chains.  
 A;Reference number: A39761; MUID:91201329; PMID:2016300  
 A;Accession: C39761  
 A;Molecule type: DNA  
 A;Residues: 1-251 <EVE>  
 R;Evensen, G.; Mathiesen, A.; Sundan, A.  
 submitted to the EMBL Data Library, October 1990  
 A;Description: Direct molecular cloning of two distinct abrin A-chains.  
 A;Reference number: S14471  
 A;Accession: S14471  
 A;Molecule type: DNA  
 A;Residues: 'M', 1-251 <EV2>  
 A;Cross-references: EMBL:X54872; NID:916088; PIDN:CAA38654.1; PID:916089  
 C;Superfamily: ricin; rRNA N-glycosidase homology  
 C;Keywords: duplication; glycosidase; hydrolase; lectin; toxin  
 F;1-251/Product: abrin (clone 7.2) chain A #status predicted <ACH>  
 F;7-246/Domain: rRNA N-glycosidase homology <RNG>  
 F;74,113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted  
 F;164,167/Active site: Glu, Arg #status predicted

Query Match 32.7%; Score 336.5; DB 2; Length 251;  
 Best Local Similarity 44.9%; Pred. No. 6.7e-23;  
 Matches 83; Conservative 24; Mismatches 69; Indels 9; Gaps 4;

QY 10 INFTAGATVQSYTNFIRAVRGRLTGDVREHPIVLPNVRGLPINQRFILVELSNHAEI 69  
 Db 5 IKSTEGATSSQYKQFIEALRERLGG--LIHDIPLVLRDPTVEERNRYITVELSNERE 62  
 QY 70 SVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDA-EAITHLFTDQVNRYYTAFGGNYDRLEQ 129  
 Db 63 SIEVGIDVTNAYVAVRAGSQSYFL---RDAPASASTLTGTQ-RYSLRFDGSGYGLER 118  
 QY 130 LAGNRENIELNGPLEAISAALYVYSGTGTLPRLARSFIIQIMISEARFQVIEG 189  
 Db 119 WAHQTEQISLIGLQALTHAIS---FLRSGANDEKARTLIVLIQMASEARFYISNRV 175  
 QY 190 RTRIR 194  
 Db 176 GVSR 180

## RESULT 11

abrin-a precursor - Indian licorice (fragment)  
 N;Contains: rRNA N-glycosidase (EC 3.2.2.22)  
 C;Species: Abrus precatorius (Indian licorice)  
 C;Date: 31-Dec-1993 #sequence\_revision 01-Aug-1997 #text\_change 16-Jul-1999  
 C;Accession: S32429; J0202; A39761; J01398; S14472; S24133; S74110; S74111  
 R;Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.  
 J. Mol. Biol. 229, 263-267, 1993  
 A;Title: Primary structure of three distinct isoabirins determined by cDNA sequencing. Cor  
 A;Reference number: S32429; MUID:93132798; PMID:8421313  
 A;Accession: S32429  
 A;Status: nucleic acid sequence not shown  
 A;Molecule type: mRNA  
 A;Residues: 'E', 2-528 <HUN>  
 A;Cross-references: GB:M88344; NID:9166294; PIDN:AAA32624.1; PID:9166295  
 A;Note: the coding region for the sequence shown is preceded by an ATG codon  
 A;Note: residues 1-8 were derived from the synthesized primer  
 R;Funatsu, G.; Taguchi, Y.; Kamenosono, M.; Yanaka, M.  
 Agric. Biol. Chem. 52, 1095-1097, 1988

A>Title: The complete amino acid sequence of the A-chain of abrin-a, a toxic protein from  
A:Reference number: JTO202  
A:Accession: JTO202  
A:Molecule type: protein  
A:Residues: 1-201,203-251 <FUN>  
A>Note: The amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have  
R:Evensen, G.; Mathiesen, A.; Sundan, A.  
J. Biol. Chem. 266, 6848-6852, 1991  
A>Title: Direct molecular cloning and expression of two distinct abrin A-chains.  
A:Reference number: A39761; MUID:91201329; PMID:2016300  
A:Accession: A39761  
A>Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 'E',2-251 <EVE>  
A:Cross-references: GB:X54872  
A>Note: residues 1-8 were derived from the synthesized primer  
R:Kimura, M.; Sumizawa, T.; Funatsu, G.  
BioSci. Biotechnol. Biochem. 57, 166-169, 1993  
A>Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, toxic  
A:Reference number: JC1398; MUID:93169023; PMID:7763422  
A:Contents: seeds  
A:Accession: JC1398  
A:Molecule type: protein  
A:Residues: 261-347,'T',349-351,'A',353-357,'L',359-528 <KIM>  
A:Experimental source: seed  
R:Evensen, G.; Mathiesen, A.; Sundan, A.  
submitted to the EMBL Data Library, October 1990  
A:Description: Direct molecular cloning of two distinct abrin A-chains.  
A:Reference number: S14471  
A:Accession: S14472  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 'ME',2-251 <EV2>  
A:Cross-references: EMBL:X54873; NID:q16090; PIDN:CAA38655.1; PID:gl6031  
R:Chen, Y.L.; Chow, L.P.; Tsugata, A.; Lin, J.Y.  
FEBS Lett. 309, 115-118, 1992  
A>Title: The complete primary structure of abrin-a B chain.  
A:Reference number: S24133; MUID:92371656; PMID:1505674  
A:Accession: S24133  
A:Molecule type: protein  
A:Residues: 262-297,'Y',299-426,'L',428-466,'P',468-482,'L',484-528 <CHE>  
R:Lin, S.H.; Chow, L.P.; Chen, Y.L.; Liaw, Y.C.; Chen, J.K.; Lin, J.Y.  
Eur. J. Biochem. 240, 564-569, 1996  
A>Title: Probing the domain structure of abrin-a by tryptic digestion.  
A:Reference number: S74110; MUID:97008945; PMID:8856055  
A:Accession: S74110  
A:Molecule type: protein  
A:Residues: 262-276,'X',278-280,329-348,369-388,399-418 <LIW>  
A:Experimental source: seed  
C:Comment: Abrin-a is more toxic than ricin. The toxin consists of an A chain, which in-  
cluding receptors on the cell surface. The A and B chains are linked by a single disulfide  
bond.  
C:Superfamily: ricin; rRNA N-glycosidase homology  
C:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglutamic acid  
F:1-251/Product: abrin-a chain A #status experimental <ACH>  
F:7-246/Domains: rRNA N-glycosidase homology <RNG>  
F:261-528/Product: abrin-a chain B #status experimental <BCH>  
F:283-325,326-366,369-407,414-449,453-492,495-528/Region: 40-residue repeats  
F:74,113,195,196/Binding site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:1/Modified site: Pyrrolidone carboxylic acid (Gln) #status predicted  
F:164,167/Active site: Glu, Arg #status predicted  
F:247-269,286-305,329-346,417-430,456-473/Disulfide bonds: #status predicted  
F:288,312/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted  
F:361,401/Binding site: Carbohydrate (Asn) (covalent) #status experimental  
F:500,521/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted

Query Match 32.0%; Score 329.5; DB 1; Length 528;  
Best Local Similarity 42.8%; Pred.No. 7.5e-22;  
Matches 80; Conservative 28; Mismatches 66; Indels 13; Gaps 5;

QY	10	INFTTAGATVQS	YTNFIRAVRGRLTTGADVRHIEIPVLPNVRGLPINQRFILVELSHAE	69
DB	5	IKFTEGATSQSYKQF	FEALRRLRG--LIHDIPVLPDPTTLQERNRYITVELSNSDTE	62
QY	70	SVTLALDVTNAYVVG	YRAGNSAYFFH--PDNQEDAEATHLFTDVQNRYYTFAFGNVDRL	127
DB	63	SIEVGIDVTNAYVAY	RAGTQSYFLRDPASSAD-----YLFCT-DQSLPFFTYGDL	116
QY	128	EOLAGNRLENELGN	GPLEEASIALSYYSYTGCTQLPTLARSFFIICMISEAAARFQYIEG	187
DB	117	ERWAHQSRQQLPLG	LQALTHGIS---FFRSGNDNEEKARTLIVIQWAEARFRYISN	173
QY	188	EMRTRIR	194	
DB	174	KRVSIQ	180	
<p>RESULT 12</p> <p>S23519</p> <p>beta-luffin - smooth loofah</p> <p>C:Species: Luffa cylindrica (smooth loofah)</p> <p>C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 20-Aug-1999</p> <p>C:Accession: S23519; S23113</p> <p>R:Kataoka, J.; Habuka, N.; Miyano, M.; Masuta, C.; Koiwai, A.</p> <p>Plant Mol. Biol. 19, 887-889, 1992</p> <p>A:Title: Nucleotide sequence of cDNA encoding beta-luffin, another ribosome-inactivating</p> <p>A:Reference number: S23519; MUID:92353400; PMID:1643290</p> <p>A:Accession: S23519</p> <p>A:Molecule type: mRNA</p> <p>A:Residues: 1-278 &lt;X&gt;</p> <p>A:Cross-references: EMBL:X62372; NID:g19149; PIDN:CAM44230.1; PID:g19150</p> <p>C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology</p> <p>F:26-264/Domain: rRNA N-glycosidase homology &lt;RNG&gt;</p>				
<p>Query Match 29.9%; Score 307.5; DB 2; Length 278;</p> <p>Best Local Similarity 35.8%; Pred. No. 3.2e-20;</p> <p>Matches 67; Conservative 45; Mismatches 64; Indels 11; Gaps 3;</p>				
QY	10	INFTTAGATVQS	YTNFIRAVRGRLTTGADVRHIEIPVLPNVRGLPINQRFILVELSHAE	69
DB	24	VFSLSGADSKSYK	FFITALRKAALPSKEKVSNIPLLLPSASGA---SRVTLMLQSLNYDAK	80
QY	70	SVTLALDVTNAYVVG	YRAGNSAYFFHDPNQEDAEATHLFTDVQNRYYTFAFGNVDRL	129
DB	81	AITMAIDVTNVI	MGVLVNSTSYFF--NESDAKLASQYVFGKSTIVTLPSYGNIERLQN	137
QY	130	LAGNRLENELGN	GPLEEASIALSYYSYTGCTQLPTLARSFFIICMISEAAARFQYIEGEM	189
DB	138	AAGKVRKEPIG	FRADFSAITSLFHYDS-----TAAGAFELVLIQTAAERFKYIEGQI	192
QY	190	RTRIRYN	196	
DB	193	IERIPKN	199	
<p>RESULT 13</p> <p>JN0108</p> <p>luffin-b - smooth loofah</p> <p>C:Species: Luffa cylindrica (smooth loofah)</p> <p>C:Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 07-May-1999</p> <p>C:Accession: JN0108</p> <p>R:Islam, M.R.; Hirayama, H.; Funatsu, G.</p> <p>Agric. Biol. Chem. 55, 229-238, 1991</p> <p>A:Title: Complete amino acid sequence of luffin-b, a ribosome-inactivating protein from</p> <p>A:Reference number: JN0108; MUID:91248488; PMID:1368666</p> <p>A:Accession: JN0108</p> <p>A&gt;Status: preliminary</p> <p>A:Molecule type: protein</p> <p>A:Residues: 1-250 &lt;LS&gt;</p> <p>C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology</p> <p>F:5-246/Domain: rRNA N-glycosidase homology &lt;RNG&gt;</p>				
<p>Query Match 29.2%; Score 300.5; DB 2; Length 250;</p>				